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(54) Title: LIGAND FOR RECEPTOR ACTIVATOR OF NF-KAPPA B, LIGAND IS MEMBER OF TNF SUPERFAMILY			
(57) Abstract  Isolated ligands, DNAs encoding such ligands, and pharmaceutical compositions made therefrom, are disclosed. The isolated ligands can be used to regulate an immune response. The ligands are also useful in screening for inhibitors thereof.			
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**TITLE**

LIGAND FOR RECEPTOR ACTIVATOR OF NF-KAPPA B, LIGAND IS MEMBER OF TNF SUPERFAMILY

**TECHNICAL FIELD OF THE INVENTION**

The present invention relates generally to the field of cytokines, and more specifically to cytokine receptor/ligand pairs having immunoregulatory activity.

**BACKGROUND OF THE INVENTION**

Efficient functioning of the immune system requires a fine balance between cell proliferation and differentiation and cell death, to ensure that the immune system is capable of reacting to foreign, but not self antigens. Integral to the process of regulating the immune and inflammatory response are various members of the Tumor Necrosis Factor (TNF) Receptor/Nerve Growth Factor Receptor superfamily (Smith et al., *Science* 248:1019, 1990). This family of receptors includes two different TNF receptors (Type I and Type II; Smith et al., *supra*; and Schall et al., *Cell* 61:361, 1990), nerve growth factor receptor (Johnson et al., *Cell* 47:545, 1986), B cell antigen CD40 (Stamenkovic et al., *EMBO J.* 8:1403, 1989), CD27 (Camerini et al., *J. Immunol.* 147:3165, 1991), CD30 (Durkop et al., *Cell* 68:421, 1992), T cell antigen OX40 (Mallett et al., *EMBO J.* 9:1063, 1990), human *Fas* antigen (Itoh et al., *Cell* 66:233, 1991), murine 4-1BB receptor (Kwon et al., *Proc. Natl. Acad. Sci. USA* 86:1963, 1989) and a receptor referred to as Apoptosis-Inducing Receptor (AIR; USSN 08/720,864, filed October 4, 1996).

CD40 is a receptor present on B lymphocytes, epithelial cells and some carcinoma cell lines that interacts with a ligand found on activated T cells, CD40L (USSN 08/249,189, filed May 24, 1994). The interaction of this ligand/receptor pair is essential for both the cellular and humoral immune response. Signal transduction via CD40 is mediated through the association of the cytoplasmic domain of this molecule with members of the TNF receptor-associated factors (TRAFs; Baker and Reddy, *Oncogene* 12:1, 1996). It has recently been found that mice that are defective in TRAF3 expression due to a targeted disruption in the gene encoding TRAF3 appear normal at birth but develop progressive hypoglycemia and depletion of peripheral white cells, and die by about ten days of age (Xu et al., *Immunity* 5:407, 1996). The immune responses of chimeric mice reconstituted with TRAF3<sup>-/-</sup> fetal liver cells resemble those of CD40-deficient mice, although TRAF3<sup>-/-</sup> B cells appear to be functionally normal.

The critical role of TRAF3 in signal transduction may be in its interaction with one of the other members of the TNF receptor superfamily, for example, CD30 or CD27.

which are present on T cells. Alternatively, there may be other, as yet unidentified members of this family of receptors that interact with TRAF3 and play an important role in postnatal development as well as in the development of a competent immune system. Identifying additional members of the TNF receptor superfamily would provide an additional means of regulating the immune and inflammatory response, as well as potentially providing further insight into post-natal development in mammals.

#### SUMMARY OF THE INVENTION

The present invention provides a counterstructure, or ligand, for a novel receptor referred to as RANK (for receptor activator of NF- $\kappa$ B), that is a member of the TNF superfamily. The ligand, which is referred to as RANKL, is a Type 2 transmembrane protein with an intracellular domain of less than about 50 amino acids, a transmembrane domain and an extracellular domain of from about 240 to 250 amino acids. Similar to other members of the TNF family to which it belongs, RANKL has a 'spacer' region between the transmembrane domain and the receptor binding domain that is not necessary for receptor binding. Accordingly, soluble forms of RANKL can comprise the entire extracellular domain or fragments thereof that include the receptor binding region.

RANK is a Type 1 transmembrane protein having 616 amino acid residues that is a member of the TNFR superfamily, and interacts with TRAF3. Triggering of RANK by over-expression, co-expression of RANK and membrane bound RANKL, or by soluble RANKL or agonistic antibodies to RANK, results in the upregulation of the transcription factor NF- $\kappa$ B, a ubiquitous transcription factor that is most extensively utilized in cells of the immune system.

These and other aspects of the present invention will become evident upon reference to the following detailed description of the invention.

#### BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 demonstrates the influence of RANK.Fc and hRANKL on activated T cell growth. Human peripheral blood T cells were cultured as described in Example 12, viable T cell recovery was determined by triplicate trypan blue countings.

Figure 2 illustrates the ability of RANKL to induce human DC cluster formation. Functionally mature dendritic cells (DC) were generated *in vitro* from CD34<sup>+</sup> bone marrow (BM) progenitors and cultured as described in Example 13. CD1a<sup>+</sup> DC were cultured in a cytokine cocktail alone (Figure 2A), in cocktail plus CD40L (Figure 2B), RANKL (Figure 2C), or heat inactivated (ΔH) RANKL (Figure 2D), and then photographed using an inversion microscope.

Figure 3 demonstrates that RANKL enhances DC allo-stimulatory capacity. Allogeneic T cells were incubated with varying numbers of irradiated DC cultured as

described in Example 13. The cultures were pulsed with [<sup>3</sup>H]-thymidine and the cells harvested onto glass fiber sheets for counting. Values represent the mean  $\pm$  standard deviation (SD) of triplicate cultures.

Figure 4 presents an alignment of human RANK with other TNFR family members in the region of structurally conserved extracellular cysteine-rich pseudorepeats. Predicted disulfide linkages (DS1-DS3) are indicated. RANK and CD40 contain identical amino acid substitutions (C<sup>\*</sup>H, C<sup>\*</sup>G) eliminating DS2 in the second pseudorepeat.

Figure 5 presents an alignment of human RANKL with other TNF family members.

#### DETAILED DESCRIPTION OF THE INVENTION

A novel partial cDNA insert with a predicted open reading frame having some similarity to CD40 was identified in a database containing sequence information from cDNAs generated from human bone marrow-derived dendritic cells (DC). The insert was used to hybridize to colony blots generated from a DC cDNA library containing full-length cDNAs. Several colony hybridizations were performed, and two clones (SEQ ID NOs: 1 and 3) were isolated. SEQ ID NO:5 shows the nucleotide and amino acid sequence of a predicted full-length protein based on alignment of the overlapping sequences of SEQ ID NOs: 1 and 3.

RANK is a member of the TNF receptor superfamily; it most closely resembles CD40 in the extracellular region. Similar to CD40, RANK associates with TRAF2 and TRAF3 (as determined by co-immunoprecipitation assays substantially as described by Rothe et al., *Cell* 83:1243, 1995). TRAFs are critically important in the regulation of the immune and inflammatory response. Through their association with various members of the TNF receptor superfamily, a signal is transduced to a cell. That signal results in the proliferation, differentiation or apoptosis of the cell, depending on which receptor(s) is/are triggered and which TRAF(s) associate with the receptor(s); different signals can be transduced to a cell via coordination of various signaling events. Thus, a signal transduced through one member of this family may be proliferative, differentiative or apoptotic, depending on other signals being transduced to the cell, and/or the state of differentiation of the cell. Such exquisite regulation of this proliferative/apoptotic pathway is necessary to develop and maintain protection against pathogens; imbalances can result in autoimmune disease.

RANK is expressed on epithelial cells, some B cell lines, and on activated T cells. However, its expression on activated T cells is late, about four days after activation. This time course of expression coincides with the expression of Fas, a known agent of apoptosis. RANK may act as an anti-apoptotic signal, rescuing cells that express RANK from apoptosis as CD40 is known to do. Alternatively, RANK may confirm an apoptotic

signal under the appropriate circumstances, again similar to CD40. RANK and its ligand are likely to play an integral role in regulation of the immune and inflammatory response.

Moreover, the post-natal lethality of mice having a targeted disruption of the TRAF3 gene demonstrates the importance of this molecule not only in the immune response but in development. The isolation of RANK, as a protein that associates with TRAF3, and its ligand, RANKL, will allow further definition of this signaling pathway, and development of diagnostic and therapeutic modalities for use in the area of autoimmune and/or inflammatory disease.

10 DNA, Proteins and Analogs

The present invention provides isolated RANKL polypeptides and analogs (or muteins) thereof having an activity exhibited by the native molecule (i.e., RANKL muteins that bind specifically to a RANK expressed on cells or immobilized on a surface or to RANKL-specific antibodies; soluble forms thereof that inhibit RANK ligand-induced signaling through RANK). Such proteins are substantially free of contaminating endogenous materials and, optionally, without associated native-pattern glycosylation. Derivatives of RANKL within the scope of the invention also include various structural forms of the primary proteins which retain biological activity. Due to the presence of ionizable amino and carboxyl groups, for example, a RANKL protein may be in the form of acidic or basic salts, or may be in neutral form. Individual amino acid residues may also be modified by oxidation or reduction. The primary amino acid structure may be modified by forming covalent or aggregative conjugates with other chemical moieties, such as glycosyl groups, lipids, phosphate, acetyl groups and the like, or by creating amino acid sequence mutants. Covalent derivatives are prepared by linking particular functional groups to amino acid side chains or at the N- or C-termini.

Derivatives of RANKL may also be obtained by the action of cross-linking agents, such as M-maleimidobenzoyl succinimide ester and N-hydroxysuccinimide, at cysteine and lysine residues. The inventive proteins may also be covalently bound through reactive side groups to various insoluble substrates, such as cyanogen bromide-activated, bisoxirane-activated, carbonyldiimidazole-activated or tosyl-activated agarose structures, or by adsorbing to polyolefin surfaces (with or without glutaraldehyde cross-linking). Once bound to a substrate, the proteins may be used to selectively bind (for purposes of assay or purification) antibodies raised against the proteins or against other proteins which are similar to RANKL, as well as other proteins that bind RANKL or homologs thereof.

35 Soluble forms of RANKL are also within the scope of the invention. The nucleotide and predicted amino acid sequence of the RANKL is shown in SEQ ID NOs:10 and 12 (murine and human, respectively). Computer analysis indicated that the RANKL is a Type 2 transmembrane protein; murine RANKL contains a predicted 48 amino acid

intracellular domain, 21 amino acid transmembrane domain and 247 amino acid extracellular domain, and human RANKL contains a predicted 47 amino acid intracellular domain, 21 amino acid transmembrane domain and 249 amino acid extracellular domain.

- 5 Soluble RANKL comprises a signal peptide and the extracellular domain or a fragment thereof. An exemplary signal peptide is that shown in SEQ ID NO:9; other signal (or leader) peptides are well-known in the art, and include that of murine Interleukin-7 or human growth hormone. RANKL is similar to other members of the TNF family in having a region of amino acids between the transmembrane domain and the receptor binding region that does not appear to be required for biological activity; this is referred to as a 'spacer' region. Amino acid sequence alignment indicates that the receptor binding region is from about amino acid 162 of human RANKL to about amino acid 317 (corresponding to amino acid 139 through 294 of murine RANKL, SEQ ID NO:10), beginning with an Ala residue that is conserved among many members of the family (amino acid 162 of SEQ ID NO:12).

- Moreover, fragments of the extracellular domain will also provide soluble forms of RANKL. Those skilled in the art will recognize that the actual receptor binding region may be different than that predicted by computer analysis. Thus, the N-terminal amino acid of a soluble RANKL is expected to be within about five amino acids on either side of the conserved Ala residue. Alternatively, all or a portion of the spacer region may be included at the N-terminus of a soluble RANKL, as may be all or a portion of the transmembrane and/or intracellular domains, provided that the resulting soluble RANKL is not membrane-associated. Accordingly, a soluble RANKL will have an N-terminal amino acid selected from the group consisting of amino acids 1 through 162 of SEQ ID NO:12 (1 through 139 of SEQ ID NO:10). Preferably, the amino terminal amino acid is between amino acids 69 and 162 of SEQ ID NO:12 (human RANKL; amino acids 48 and 139 of SEQ ID NO:10). Similarly, the carboxy terminal amino acid can be between amino acid 313 and 317 of SEQ ID NO:12 (human RANKL; corresponding to amino acids 290 through 294 of SEQ ID NO:10). Those skilled in the art can prepare these and additional soluble forms through routine experimentation.

- Fragments can be prepared using known techniques to isolate a desired portion of the extracellular region, and can be prepared, for example, by comparing the extracellular region with those of other members of the TNF family (of which RANKL is a member) and selecting forms similar to those prepared for other family members. Alternatively, unique restriction sites or PCR techniques that are known in the art can be used to prepare numerous truncated forms which can be expressed and analyzed for activity.

- 35 Other derivatives of the RANKL proteins within the scope of this invention include covalent or aggregative conjugates of the proteins or their fragments with other proteins or polypeptides, such as by synthesis in recombinant culture as N-terminal or C-terminal fusions. For example, the conjugated peptide may be a signal (or leader) polypeptide

sequence at the N-terminal region of the protein which co-translationally or post-translationally directs transfer of the protein from its site of synthesis to its site of function inside or outside of the cell membrane or wall (e.g., the yeast  $\alpha$ -factor leader).

- Protein fusions can comprise peptides added to facilitate purification or
- 5 identification of RANKL proteins and homologs (e.g., poly-His). The amino acid sequence of the inventive proteins can also be linked to an identification peptide such as that described by Hopp et al., *BioTechnology* 6:1204 (1988). Such a highly antigenic peptide provides an epitope reversibly bound by a specific monoclonal antibody, enabling rapid
- 10 assay and facile purification of expressed recombinant protein. The sequence of Hopp et al. is also specifically cleaved by bovine mucosal enterokinase, allowing removal of the peptide from the purified protein. Fusion proteins capped with such peptides may also be resistant to intracellular degradation in *E. coli*.

- Fusion proteins further comprise the amino acid sequence of a RANKL linked to an immunoglobulin Fc region. An exemplary Fc region is a human IgG, having a nucleotide
- 15 an amino acid sequence set forth in SEQ ID NO:8. Fragments of an Fc region may also be used, as can Fc mutants. For example, certain residues within the hinge region of an Fc region are critical for high affinity binding to Fc $\gamma$ RI. Canfield and Morrison (*J. Exp. Med.* 173:1483; 1991) reported that Leu4234 and Leu4235 were critical to high affinity binding of IgG<sub>3</sub> to Fc $\gamma$ RI present on U937 cells. Similar results were obtained by Lund et al. (*J. Immunol.* 147:2657, 1991; *Molecular Immunol.* 29:53, 1991). Such mutations, alone or
- 20 in combination, can be made in an IgG Fc region to decrease the affinity of IgG for FcR. Depending on the portion of the Fc region used, a fusion protein may be expressed as a dimer, through formation of interchain disulfide bonds. If the fusion proteins are made with both heavy and light chains of an antibody, it is possible to form a protein oligomer
- 25 with as many as four RANKL regions.

- In another embodiment, RANKL proteins further comprise an oligomerizing peptide such as a leucine zipper domain. Leucine zippers were originally identified in several DNA-binding proteins (Landschulz et al., *Science* 240:1759, 1988). Leucine zipper domain is a term used to refer to a conserved peptide domain present in these (and
- 30 other) proteins, which is responsible for dimerization of the proteins. The leucine zipper domain (also referred to herein as an oligomerizing, or oligomer-forming, domain) comprises a repetitive heptad repeat, with four or five leucine residues interspersed with other amino acids. Examples of leucine zipper domains are those found in the yeast transcription factor GCN4 and a heat-stable DNA-binding protein found in rat liver (C/EBP; Landschulz et al., *Science* 243:1681, 1989). Two nuclear transforming proteins, *fos* and *jun*, also exhibit leucine zipper domains, as does the gene product of the murine proto-oncogene, *c-myc* (Landschulz et al., *Science* 240:1759, 1988). The products of the nuclear oncogenes *fos* and *jun* comprise leucine zipper domains preferentially form a
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heterodimer (O'Shea et al., *Science* 245:646, 1989; Turner and Tjian, *Science* 243:1689, 1989). The leucine zipper domain is necessary for biological activity (DNA binding) in these proteins.

- The fusogenic proteins of several different viruses, including paramyxovirus, coronavirus, measles virus and many retroviruses, also possess leucine zipper domains (Buckland and Wild, *Nature* 338:547, 1989; Britton, *Nature* 353:394, 1991; Delwart and Mosialos, *AIDS Research and Human Retroviruses* 6:703, 1990). The leucine zipper domains in these fusogenic viral proteins are near the transmembrane region of the proteins; it has been suggested that the leucine zipper domains could contribute to the oligomeric structure of the fusogenic proteins. Oligomerization of fusogenic viral proteins is involved in fusion pore formation (Spruce et al, *Proc. Natl. Acad. Sci. U.S.A.* 88:3523, 1991). Leucine zipper domains have also been recently reported to play a role in oligomerization of heat-shock transcription factors (Rabindran et al., *Science* 259:230, 1993).

- Leucine zipper domains fold as short, parallel coiled coils. (O'Shea et al., *Science* 254:539, 1991) The general architecture of the parallel coiled coil has been well characterized, with a "knobs-into-holes" packing as proposed by Crick in 1953 (*Acta Crystallogr.* 6:689). The dimer formed by a leucine zipper domain is stabilized by the heptad repeat, designated *(abcdefg)<sub>n</sub>* according to the notation of McLachlan and Stewart (*J. Mol. Biol.* 98:293, 1975), in which residues *a* and *d* are generally hydrophobic residues, with *d* being a leucine, which line up on the same face of a helix. Oppositely-charged residues commonly occur at positions *g* and *e*. Thus, in a parallel coiled coil formed from two helical leucine zipper domains, the "knobs" formed by the hydrophobic side chains of the first helix are packed into the "holes" formed between the side chains of the second helix.

- The leucine residues at position *d* contribute large hydrophobic stabilization energies, and are important for dimer formation (Krystek et al., *Int. J. Peptide Res.* 38:229, 1991). Lovejoy et al. recently reported the synthesis of a triple-stranded  $\alpha$ -helical bundle in which the helices run up-up-down (*Science* 259:1288, 1993). Their studies confirmed that hydrophobic stabilization energy provides the main driving force for the formation of coiled coils from helical monomers. These studies also indicate that electrostatic interactions contribute to the stoichiometry and geometry of coiled coils.

- Several studies have indicated that conservative amino acids may be substituted for individual leucine residues with minimal decrease in the ability to dimerize; multiple changes, however, usually result in loss of this ability (Landschutz et al., *Science* 243:1681, 1989; Turner and Tjian, *Science* 243:1689, 1989; Hu et al., *Science* 250:1400, 1990). van Heckeran et al. reported that a number of different amino residues can be substituted for the leucine residues in the leucine zipper domain of GCN4, and further found that some GCN4 proteins containing two leucine substitutions were weakly active

(*Nucl. Acids Res.* 20:3721, 1992). Mutation of the first and second heptad leucines of the leucine zipper domain of the measles virus fusion protein (MVF) did not affect syncytium formation (a measure of virally-induced cell fusion); however, mutation of all four leucine residues prevented fusion completely (Buckland et al., *J. Gen. Virol.* 73:1703, 1992). None of the mutations affected the ability of MVF to form a tetramer.

Amino acid substitutions in the *a* and *d* residues of a synthetic peptide representing the GCN4 leucine zipper domain have been found to change the oligomerization properties of the leucine zipper domain (Alber, Sixth Symposium of the Protein Society, San Diego, CA). When all residues at position *a* are changed to isoleucine, the leucine zipper still forms a parallel dimer. When, in addition to this change, all leucine residues at position *d* are also changed to isoleucine, the resultant peptide spontaneously forms a trimeric parallel coiled coil in solution. Substituting all amino acids at position *d* with isoleucine and at position *a* with leucine results in a peptide that tetramerizes. Peptides containing these substitutions are still referred to as leucine zipper domains.

The present invention also includes RANKL with or without associated native-pattern glycosylation. Proteins expressed in yeast or mammalian expression systems, e.g., COS-7 cells, may be similar or slightly different in molecular weight and glycosylation pattern than the native molecules, depending upon the expression system. Expression of DNAs encoding the inventive proteins in bacteria such as *E. coli* provides non-glycosylated molecules. Functional mutant analogs of RANKL protein having inactivated N-glycosylation sites can be produced by oligonucleotide synthesis and ligation or by site-specific mutagenesis techniques. These analog proteins can be produced in a homogeneous, reduced-carbohydrate form in good yield using yeast expression systems. N-glycosylation sites in eukaryotic proteins are characterized by the amino acid triplet Asn-*A<sub>i</sub>*-Z, where *A<sub>i</sub>* is any amino acid except Pro, and Z is Ser or Thr. In this sequence, asparagine provides a side chain amino group for covalent attachment of carbohydrate. Such a site can be eliminated by substituting another amino acid for Asn or for residue Z, deleting Asn or Z, or inserting a non-Z amino acid between *A<sub>i</sub>* and Z, or an amino acid other than Asn between Asn and *A<sub>i</sub>*.

RANKL protein derivatives may also be obtained by mutations of the native RANKL or subunits thereof. A RANKL mutated protein, as referred to herein, is a polypeptide homologous to a native RANKL protein, but which has an amino acid sequence different from the native protein because of one or a plurality of deletions, insertions or substitutions. The effect of any mutation made in a DNA encoding a mutated peptide may be easily determined by analyzing the ability of the mutated peptide to bind its counterstructure in a specific manner. Moreover, activity of RANKL analogs, muteins or

derivatives can be determined by any of the assays described herein (for example, induction of NF- $\kappa$ B activation).

Analogues of the inventive proteins may be constructed by, for example, making various substitutions of residues or sequences or deleting terminal or internal residues or sequences not needed for biological activity. For example, cysteine residues can be deleted or replaced with other amino acids to prevent formation of incorrect intramolecular disulfide bridges upon renaturation. Other approaches to mutagenesis involve modification of adjacent dibasic amino acid residues to enhance expression in yeast systems in which KEX2 protease activity is present.

- 10 When a deletion or insertion strategy is adopted, the potential effect of the deletion or insertion on biological activity should be considered. Subunits of the inventive proteins may be constructed by deleting terminal or internal residues or sequences. Soluble forms of RANKL can be readily prepared and tested for their ability to induce NF- $\kappa$ B activation. Polypeptides corresponding to the cytoplasmic regions, and fragments thereof (for example, a death domain) can be prepared by similar techniques. Additional guidance as to the types of mutations that can be made is provided by a comparison of the sequence of RANKL to proteins that have similar structures, as well as by performing structural analysis of the inventive RANKL proteins.

- 15 Generally, substitutions should be made conservatively; i.e., the most preferred substitute amino acids are those which do not affect the biological activity of RANKL (i.e., ability of the inventive proteins to bind antibodies to the corresponding native protein in substantially equivalent a manner, the ability to bind the counterstructure in substantially the same manner as the native protein, the ability to induce a RANKL signal, or ability to induce NF- $\kappa$ B activation). Examples of conservative substitutions include substitution of amino acids outside of the binding domain(s) (either ligand/receptor or antibody binding areas for the extracellular domain, or regions that interact with other, intracellular proteins for the cytoplasmic domain), and substitution of amino acids that do not alter the secondary and/or tertiary structure of the native protein. Additional examples include substituting one aliphatic residue for another, such as Ile, Val, Leu, or Ala for one another, or substitutions of one polar residue for another, such as between Lys and Arg; Glu and Asp; or Gln and Asn. Other such conservative substitutions, for example, substitutions of entire regions having similar hydrophobicity characteristics, are well known.

- 20 Mutations in nucleotide sequences constructed for expression of analog proteins or fragments thereof must, of course, preserve the reading frame phase of the coding sequences and preferably will not create complementary regions that could hybridize to produce secondary mRNA structures such as loops or hairpins which would adversely affect translation of the mRNA.

Not all mutations in the nucleotide sequence which encodes a RANKL protein or fragments thereof will be expressed in the final product, for example, nucleotide substitutions may be made to enhance expression, primarily to avoid secondary structure loops in the transcribed mRNA (see EPA 75,444A, incorporated herein by reference), or to provide codons that are more readily translated by the selected host, e.g., the well-known *E. coli* preference codons for *E. coli* expression.

Although a mutation site may be predetermined, it is not necessary that the nature of the mutation *per se* be predetermined. For example, in order to select for optimum characteristics of mutants, random mutagenesis may be conducted and the expressed mutated proteins screened for the desired activity. Mutations can be introduced at particular loci by synthesizing oligonucleotides containing a mutant sequence, flanked by restriction sites enabling ligation to fragments of the native sequence. Following ligation, the resulting reconstructed sequence encodes an analog having the desired amino acid insertion, substitution, or deletion.

Alternatively, oligonucleotide-directed site-specific mutagenesis procedures can be employed to provide an altered gene having particular codons altered according to the substitution, deletion, or insertion required. Exemplary methods of making the alterations set forth above are disclosed by Walder et al. (*Gene* 42:133, 1986); Bauer et al. (*Gene* 37:73, 1985); Craik (*BioTechniques*, January 1985, 12-19); Smith et al. (*Genetic Engineering: Principles and Methods*, Plenum Press, 1981); and U.S. Patent NOs. 4,518,584 and 4,737,462 disclose suitable techniques, and are incorporated by reference herein.

Additional embodiments of the inventive proteins include RANKL polypeptides encoded by DNAs capable of hybridizing to the DNAs of SEQ ID NO:10 or 12 under moderately stringent conditions (prewashing solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0) and hybridization conditions of 50°C, 5 X SSC, overnight) to the DNA sequences encoding RANKL, or more preferably under stringent conditions (for example, hybridization in 6 X SSC at 63°C overnight; washing in 3 X SSC at 55°C), and other sequences which are degenerate to those which encode the RANKL. In one embodiment, RANKL polypeptides are at least about 70% identical in amino acid sequence to the amino acid sequence of native RANKL protein as set forth in SEQ ID NOs:10 and 12. In a preferred embodiment, RANKL polypeptides are at least about 80% identical in amino acid sequence to the native form of RANKL; most preferred polypeptides are those that are at least about 90% identical to native RANKL.

Percent identity may be determined using a computer program, for example, the GAP computer program described by Devereux et al. (*Nucl. Acids Res.* 12:387, 1984) and available from the University of Wisconsin Genetics Computer Group (UWCGC). For

fragments derived from the RANKL protein, the identity is calculated based on that portion of the RANKL protein that is present in the fragment

The biological activity of RANKL analogs or muteins can be determined by testing the ability of the analogs or muteins to induce a signal through RANK, for example, activation of transcription as described in the Examples herein. Alternatively, suitable assays, for example, an enzyme immunoassay or a dot blot, employing an antibody that binds native RANKL, or a soluble form of RANK, can be used to assess the activity of RANKL analogs or muteins. Suitable assays also include, for example, assays that measure the ability of a RANKL peptide or mutein to bind cells expressing RANK, and/or the biological effects thereon. Such methods are well known in the art.

Fragments of the RANKL nucleotide sequences are also useful. In one embodiment, such fragments comprise at least about 17 consecutive nucleotides, preferably at least about 25 nucleotides, more preferably at least 30 consecutive nucleotides, of the RANKL DNA disclosed herein. DNA and RNA complements of such fragments are provided herein, along with both single-stranded and double-stranded forms of the RANKL DNAs of SEQ ID NOs:10 and 12, and those encoding the aforementioned polypeptides. A fragment of RANKL DNA generally comprises at least about 17 nucleotides, preferably from about 17 to about 30 nucleotides. Such nucleic acid fragments (for example, a probe corresponding to the extracellular domain of RANKL) are used as a probe or as primers in a polymerase chain reaction (PCR).

The probes also find use in detecting the presence of RANKL nucleic acids in *in vitro* assays and in such procedures as Northern and Southern blots. Cell types expressing RANKL can be identified as well. Such procedures are well known, and the skilled artisan can choose a probe of suitable length, depending on the particular intended application. For PCR, 5' and 3' primers corresponding to the termini of a desired RANKL DNA sequence are employed to amplify that sequence, using conventional techniques.

Other useful fragments of the RANKL nucleic acids are antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target RANKL mRNA (sense) or RANKL DNA (antisense) sequences. The ability to create an antisense or a sense oligonucleotide, based upon a cDNA sequence for a given protein is described in, for example, Stein and Cohen, *Cancer Res.* 48:2659, 1988 and van der Krol et al., *BioTechniques* 6:958, 1988.

#### Uses of DNAs, Proteins and Analogs

The RANKL DNAs, proteins and analogs described herein will have numerous uses, including the preparation of pharmaceutical compositions. For example, soluble forms of RANKL will be useful to transduce signal via RANK. RANKL compositions (both protein and DNAs) will also be useful in development of antibodies to RANKL, both

those that inhibit binding to RANK and those that do not. The inventive DNAs are useful for the expression of recombinant proteins, and as probes for analysis (either quantitative or qualitative) of the presence or distribution of RANKL transcripts.

The inventive proteins will also be useful in preparing kits that are used to detect soluble RANK or RANKL, or monitor RANK-related activity, for example, in patient specimens. RANKL proteins will also find uses in monitoring RANK-related activity in other samples or compositions, as is necessary when screening for antagonists or mimetics of this activity (for example, peptides or small molecules that inhibit or mimic, respectively, the interaction). A variety of assay formats are useful in such kits, including (but not limited to) ELISA, dot blot, solid phase binding assays (such as those using a biosensor), rapid format assays and bioassays.

The purified RANKL according to the invention will facilitate the discovery of inhibitors of RANK, and thus, inhibitors of an inflammatory response (via inhibition of NF- $\kappa$ B activation). The use of a purified RANKL polypeptide in the screening for potential inhibitors is important and can virtually eliminate the possibility of interfering reactions with contaminants. Such a screening assay can utilize either the extracellular domain of RANKL, or a fragment thereof. Detecting the inhibiting activity of a molecule would typically involve use of a soluble form of RANKL derived from the extracellular domain in a screening assay to detect molecules capable of binding RANK and inhibiting binding of the RANKL.

In addition, RANKL polypeptides can also be used for structure-based design of RANKL-inhibitors. Such structure-based design is also known as "rational drug design." The RANKL polypeptides can be three-dimensionally analyzed by, for example, X-ray crystallography, nuclear magnetic resonance or homology modeling, all of which are well-known methods. The use of RANKL structural information in molecular modeling software systems to assist in inhibitor design is also encompassed by the invention. Such computer-assisted modeling and drug design may utilize information such as chemical conformational analysis, electrostatic potential of the molecules, protein folding, etc. A particular method of the invention comprises analyzing the three dimensional structure of RANKL for likely binding sites of substrates, synthesizing a new molecule that incorporates a predictive reactive site, and assaying the new molecule as described above.

Moreover, as shown in the Examples herein, soluble forms of RANKL will be useful to induce maturation of dendritic cells (DC), and to enhance their allo-stimulatory capacity. Accordingly, RANKL proteins will be useful in augmenting an immune response, and can be used for these purposes either ex vivo (i.e., in obtaining cells such as DC from an individual, exposing them to antigen and cytokines ex vivo, and re-administering them to the individual) or in vivo (i.e., as a vaccine adjuvant that will augment humoral and/or cellular immunity). RANKL will also be useful promoting

viability of T cells in the presence of TGF $\beta$ , which will also be helpful in regulating an immune response.

#### Expression of Recombinant RANKL

5       The proteins of the present invention are preferably produced by recombinant DNA methods by inserting a DNA sequence encoding RANKL protein or an analog thereof into a recombinant expression vector and expressing the DNA sequence in a recombinant expression system under conditions promoting expression. DNA sequences encoding the proteins provided by this invention can be assembled from cDNA fragments and short  
10       oligonucleotide linkers, or from a series of oligonucleotides, to provide a synthetic gene which is capable of being inserted in a recombinant expression vector and expressed in a recombinant transcriptional unit.

15       Recombinant expression vectors include synthetic or cDNA-derived DNA fragments encoding RANKL, or homologs, mutants or bioequivalent analogs thereof, operably linked to suitable transcriptional or translational regulatory elements derived from mammalian, microbial, viral or insect genes. Such regulatory elements include a transcriptional promoter, an optional operator sequence to control transcription, a sequence encoding suitable mRNA ribosomal binding sites, and sequences which control the termination of transcription and translation, as described in detail below. The ability to  
20       replicate in a host, usually conferred by an origin of replication, and a selection gene to facilitate recognition of transformants may additionally be incorporated.

      DNA regions are operably linked when they are functionally related to each other. For example, DNA for a signal peptide (secretory leader) is operably linked to DNA for a polypeptide if it is expressed as a precursor which participates in the secretion of the  
25       polypeptide; a promoter is operably linked to a coding sequence if it controls the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to permit translation. Generally, operably linked means contiguous and, in the case of secretory leaders, contiguous and in reading frame. DNA sequences encoding RANKL, or homologs or analogs thereof which are to be expressed in  
30       a microorganism will preferably contain no introns that could prematurely terminate transcription of DNA into mRNA.

      Useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such  
35       commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and pGEM1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. *E. coli* is typically transformed using derivatives of pBR322, a plasmid derived

from an *E. coli* species (Bolivar et al., *Gene* 2:95, 1977). pBR322 contains genes for ampicillin and tetracycline resistance and thus provides simple means for identifying transformed cells.

- Promoters commonly used in recombinant microbial expression vectors include the  $\beta$ -lactamase (penicillinase) and lactose promoter system (Chang et al., *Nature* 275:615, 1978; and Goeddel et al., *Nature* 281:544, 1979), the tryptophan (trp) promoter system (Goeddel et al., *Nucl. Acids Res.* 8:4057, 1980; and EPA 36,776) and tac promoter (Maniatis, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, p. 412, 1982). A particularly useful bacterial expression system employs the phage  $\lambda$  PL promoter and cI857ts thermolabile repressor. Plasmid vectors available from the American Type Culture Collection which incorporate derivatives of the  $\lambda$  PL promoter include plasmid pHUB2, resident in *E. coli* strain JMB9 (ATCC 37092) and pPLc28, resident in *E. coli* RR1 (ATCC 53082).
- Suitable promoter sequences in yeast vectors include the promoters for metallothionein, 3-phosphoglycerate kinase (Hitzeman et al., *J. Biol. Chem.* 255:2073, 1980) or other glycolytic enzymes (Hess et al., *J. Adv. Enzyme Reg.* 7:149, 1968; and Holland et al., *Biochem.* 17:4900, 1978), such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase. Suitable vectors and promoters for use in yeast expression are further described in R. Hitzeman et al., EPA 73,657.

- Preferred yeast vectors can be assembled using DNA sequences from pBR322 for selection and replication in *E. coli* (Amp<sup>r</sup> gene and origin of replication) and yeast DNA sequences including a glucose-repressible ADH2 promoter and  $\alpha$ -factor secretion leader.
- The ADH2 promoter has been described by Russell et al. (*J. Biol. Chem.* 258:2674, 1982) and Beier et al. (*Nature* 300:724, 1982). The yeast  $\alpha$ -factor leader, which directs secretion of heterologous proteins, can be inserted between the promoter and the structural gene to be expressed. See, e.g., Kurjan et al., *Cell* 30:933, 1982; and Bitter et al., *Proc. Natl. Acad. Sci. USA* 81:5330, 1984. The leader sequence may be modified to contain, near its 3' end, one or more useful restriction sites to facilitate fusion of the leader sequence to foreign genes.

- The transcriptional and translational control sequences in expression vectors to be used in transforming vertebrate cells may be provided by viral sources. For example, commonly used promoters and enhancers are derived from Polyoma, Adenovirus 2, Simian Virus 40 (SV40), and human cytomegalovirus. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early and late promoter, enhancer, splice, and polyadenylation sites may be used to provide the other genetic elements required for expression of a heterologous DNA sequence. The early and late promoters are particularly



useful because both are obtained easily from the virus as a fragment which also contains the SV40 viral origin of replication (Fiers et al., *Nature* 273:113, 1978). Smaller or larger SV40 fragments may also be used, provided the approximately 250 bp sequence extending from the *Hind* III site toward the *Bgl* II site located in the viral origin of replication is included. Further, viral genomic promoter, control and/or signal sequences may be utilized, provided such control sequences are compatible with the host cell chosen. Exemplary vectors can be constructed as disclosed by Okayama and Berg (*Mol. Cell. Biol.* 3:280, 1983).

- A useful system for stable high level expression of mammalian receptor cDNAs in C127 murine mammary epithelial cells can be constructed substantially as described by Cosman et al. (*Mol. Immunol.* 23:935, 1986). A preferred eukaryotic vector for expression of RANKL DNA is referred to as pDC406 (McMahan et al., *EMBO J.* 10:2821, 1991), and includes regulatory sequences derived from SV40, human immunodeficiency virus (HIV), and Epstein-Barr virus (EBV). Other preferred vectors include pDC409 and pDC410, which are derived from pDC406. pDC410 was derived from pDC406 by substituting the EBV origin of replication with sequences encoding the SV40 large T antigen. pDC409 differs from pDC406 in that a *Bgl* II restriction site outside of the multiple cloning site has been deleted, making the *Bgl* II site within the multiple cloning site unique.

- A useful cell line that allows for episomal replication of expression vectors, such as pDC406 and pDC409, which contain the EBV origin of replication, is CV-1/EBNA (ATCC CRL 10478). The CV-1/EBNA cell line was derived by transfection of the CV-1 cell line with a gene encoding Epstein-Barr virus nuclear antigen-1 (EBNA-1) and constitutively express EBNA-1 driven from human CMV immediate-early enhancer/promoter.

#### Host Cells

- Transformed host cells are cells which have been transformed or transfected with expression vectors constructed using recombinant DNA techniques and which contain sequences encoding the proteins of the present invention. Transformed host cells may express the desired protein (RANKL, or homologs or analogs thereof), but host cells transformed for purposes of cloning or amplifying the inventive DNA do not need to express the protein. Expressed proteins will preferably be secreted into the culture supernatant, depending on the DNA selected, but may be deposited in the cell membrane.

- Suitable host cells for expression of proteins include prokaryotes, yeast or higher eukaryotic cells under the control of appropriate promoters. Prokaryotes include gram negative or gram positive organisms, for example *E. coli* or *Bacillus* spp. Higher eukaryotic cells include established cell lines of mammalian origin as described below. Cell-free translation systems could also be employed to produce proteins using RNAs

derived from the DNA constructs disclosed herein. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts are described by Pourwels et al. (*Cloning Vectors: A Laboratory Manual*, Elsevier, New York, 1985), the relevant disclosure of which is hereby incorporated by reference.

- 5 Prokaryotic expression hosts may be used for expression of RANKL, or homologs or analogs thereof that do not require extensive proteolytic and disulfide processing. Prokaryotic expression vectors generally comprise one or more phenotypic selectable markers, for example a gene encoding proteins conferring antibiotic resistance or supplying an autotrophic requirement, and an origin of replication recognized by the host to ensure  
10 amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium*, and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

- Recombinant RANKL may also be expressed in yeast hosts, preferably from the  
15 *Saccharomyces* species, such as *S. cerevisiae*. Yeast of other genera, such as *Pichia* or *Kluyveromyces* may also be employed. Yeast vectors will generally contain an origin of replication from the 2 $\mu$  yeast plasmid or an autonomously replicating sequence (ARS), promoter, DNA encoding the protein, sequences for polyadenylation and transcription termination and a selection gene. Preferably, yeast vectors will include an origin of  
20 replication and selectable marker permitting transformation of both yeast and *E. coli*, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* trp1 gene, which provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, and a promoter derived from a highly expressed yeast gene to induce transcription of a structural sequence downstream. The presence of the trp1 lesion in the yeast host cell genome then  
25 provides an effective environment for detecting transformation by growth in the absence of tryptophan.

- Suitable yeast transformation protocols are known to those of skill in the art; an exemplary technique is described by Hinnen et al., *Proc. Natl. Acad. Sci. USA* 75:1929, 1978, selecting for Trp<sup>+</sup> transformants in a selective medium consisting of 0.67% yeast  
30 nitrogen base, 0.5% casamino acids, 2% glucose, 10  $\mu$ g/ml adenine and 20  $\mu$ g/ml uracil. Host strains transformed by vectors comprising the ADH2 promoter may be grown for expression in a rich medium consisting of 1% yeast extract, 2% peptone, and 1% glucose supplemented with 80  $\mu$ g/ml adenine and 80  $\mu$ g/ml uracil. Derepression of the ADH2 promoter occurs upon exhaustion of medium glucose. Crude yeast supernatants are  
35 harvested by filtration and held at 4°C prior to further purification.

Various mammalian or insect cell culture systems can be employed to express recombinant protein. Baculovirus systems for production of heterologous proteins in insect cells are reviewed by Luckow and Summers, *BioTechnology* 6:47 (1988). Examples of

suitable mammalian host cell lines include the COS-7 lines of monkey kidney cells, described by Gluzman (*Cell* 23:175, 1981), and other cell lines capable of expressing an appropriate vector including, for example, CV-1/EBNA (ATCC CRL 10478), L cells, C127, 3T3, Chinese hamster ovary (CHO), HeLa and BHK cell lines. Mammalian expression vectors may comprise nontranscribed elements such as an origin of replication, a suitable promoter and enhancer linked to the gene to be expressed, and other 5' or 3' flanking nontranscribed sequences, and 5' or 3' nontranslated sequences, such as necessary ribosome binding sites, a polyadenylation site, splice donor and acceptor sites, and transcriptional termination sequences.

#### Purification of Recombinant RANKL

Purified RANKL, and homologs or analogs thereof are prepared by culturing suitable host/vector systems to express the recombinant translation products of the DNAs of the present invention, which are then purified from culture media or cell extracts. For example, supernatants from systems which secrete recombinant protein into culture media can be first concentrated using a commercially available protein concentration filter, for example, an Amicon or Millipore Pellicon ultrafiltration unit.

Following the concentration step, the concentrate can be applied to a suitable purification matrix. For example, a suitable affinity matrix can comprise a counter structure protein or lectin or antibody molecule bound to a suitable support. Alternatively, an anion exchange resin can be employed, for example, a matrix or substrate having pendant diethylaminoethyl (DEAE) groups. The matrices can be acrylamide, agarose, dextran, cellulose or other types commonly employed in protein purification. Alternatively, a cation exchange step can be employed. Suitable cation exchangers include various insoluble matrices comprising sulfopropyl or carboxymethyl groups. Sulfopropyl groups are preferred. Gel filtration chromatography also provides a means of purifying the inventive proteins.

Affinity chromatography is a particularly preferred method of purifying RANKL and homologs thereof. For example, a RANKL expressed as a fusion protein comprising an immunoglobulin Fc region can be purified using Protein A or Protein G affinity chromatography. Moreover, a RANKL protein comprising an oligomerizing zipper domain may be purified on a resin comprising an antibody specific to the oligomerizing zipper domain. Monoclonal antibodies against the RANKL protein may also be useful in affinity chromatography purification, by utilizing methods that are well-known in the art. A ligand may also be used to prepare an affinity matrix for affinity purification of RANKL.

Finally, one or more reversed-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify a RANKL composition.

Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a homogeneous recombinant protein.

Recombinant protein produced in bacterial culture is usually isolated by initial extraction from cell pellets, followed by one or more concentration, salting-out, aqueous ion exchange or size exclusion chromatography steps. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of recombinant protein can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

- 10 Fermentation of yeast which express the inventive protein as a secreted protein greatly simplifies purification. Secreted recombinant protein resulting from a large-scale fermentation can be purified by methods analogous to those disclosed by Urdal et al. (*J. Chromatog.* 296:171, 1984). This reference describes two sequential, reversed-phase HPLC steps for purification of recombinant human GM-CSF on a preparative HPLC column.

15 Protein synthesized in recombinant culture is characterized by the presence of cell components, including proteins, in amounts and of a character which depend upon the purification steps taken to recover the inventive protein from the culture. These components ordinarily will be of yeast, prokaryotic or non-human higher eukaryotic origin and preferably are present in innocuous contaminant quantities, on the order of less than about 1 percent by weight. Further, recombinant cell culture enables the production of the inventive proteins free of other proteins which may be normally associated with the proteins as they are found in nature in the species of origin.

#### 25 Uses and Administration of RANKL Compositions

The present invention provides methods of using therapeutic compositions comprising an effective amount of a protein and a suitable diluent and carrier, and methods for regulating an immune or inflammatory response. The use of RANKL in conjunction with soluble cytokine receptors or cytokines, or other immunoregulatory molecules is also contemplated.

30 For therapeutic use, purified protein is administered to a patient, preferably a human, for treatment in a manner appropriate to the indication. Thus, for example, RANKL protein compositions administered to regulate immune function can be given by bolus injection, continuous infusion, sustained release from implants, or other suitable technique. Typically, a therapeutic agent will be administered in the form of a composition comprising purified RANKL, in conjunction with physiologically acceptable carriers, excipients or diluents. Such carriers will be nontoxic to recipients at the dosages and concentrations employed.

Ordinarily, the preparation of such protein compositions entails combining the inventive protein with buffers, antioxidants such as ascorbic acid, low molecular weight (less than about 10 residues) polypeptides, proteins, amino acids, carbohydrates including glucose, sucrose or dextrans, chelating agents such as EDTA, glutathione and other

- 5 stabilizers and excipients. Neutral buffered saline or saline mixed with conspecific serum albumin are exemplary appropriate diluents. Preferably, product is formulated as a lyophilizate using appropriate excipient solutions (e.g., sucrose) as diluents. Appropriate dosages can be determined in trials. The amount and frequency of administration will depend, of course, on such factors as the nature and severity of the indication being treated,
- 10 the desired response, the condition of the patient, and so forth.

As shown herein, RANKL has beneficial effects on various cells important in the immune system. Accordingly, RANKL may be administered to an individual as a vaccine adjuvant, or as a therapeutic agent to upregulate an immune response, for example, infectious disease. Moreover, NF- $\kappa$ B has been found to play a protective role in

15 preventing apoptotic death of cells induced by TNF- $\alpha$  or chemotherapy. Accordingly, agonists of RANK (i.e., RANKL and agonistic antibodies) will be useful in protecting RANK-expressing cells from the negative effects of chemotherapy or the presence of high levels of TNF- $\alpha$  such as occur in sepsis (see, i.e., Barinaga, *Science* 274:724, 1996, and the articles by Beg and Baltimore and Wang et al., pages 782 and 784 of that same issue of

20 *Science*).

Throughout the description and claims of this specification, the word "comprise" and variations of the word, such as "comprising" and "comprises", is

25 not intended to exclude other additives, components, integers or steps.

The following examples are offered by way of illustration, and not by way of limitation. Those skilled in the art will recognize that variations of the invention embodied in the examples can be made, especially in light of the teachings of the

30 various references cited herein, the disclosures of which are incorporated by reference.

#### EXAMPLE 1

- 30 The example describes the identification and isolation of a DNA encoding a novel member of the TNF receptor superfamily. A partial cDNA insert with a predicted open reading frame having some similarity to CD40 (a cell-surface antigen present on the surface of both normal and neoplastic human B cells that has been shown to play an important role in B-cell proliferation and differentiation; Stamenkovic et al., *EMBO J.* 8:1403, 1989),
- 35 was identified in a database containing sequence information from cDNAs generated from human bone marrow-derived dendritic cells (DC). The insert was excised from the vector by restriction endonuclease digestion, gel purified, labeled with  $^{32}$ P, and used to hybridize to colony blots generated from a DC cDNA library containing larger cDNA inserts using



high stringency hybridization and washing techniques (hybridization in 5xSSC, 50% formamide at 42°C overnight, washing in 0.5xSSC at 63°C); other suitable high stringency conditions are disclosed in Sambrook et al. in *Molecular Cloning: A Laboratory Manual*, 2nd ed. (Cold Spring Harbor Laboratory, Cold Spring Harbor, NY: 1989), 9.52-9.55.

- 5 Initial experiments yielded a clone referred to as 9D-8A (SEQ ID NO:1); subsequent analysis indicated that this clone contained all but the extreme 5' end of a novel cDNA, with predicted intron sequence at the extreme 5' end (nucleotides 1-92 of SEQ ID NO:1). Additional colony hybridizations were performed, and a second clone was isolated. The second clone, referred to as 9D-15C (SEQ ID NO:3), contained the 5' end without intron interruption but not the full 3' end. SEQ ID NO:5 shows the nucleotide and amino acid sequence of a predicted full-length protein based on alignment of the overlapping sequences of SEQ ID NOs:1 and 3.
- 10

- The encoded protein was designated RANK, for receptor activator of NF- $\kappa$ B. The cDNA encodes a predicted Type I transmembrane protein having 616 amino acid residues, with a predicted 24 amino acid signal sequence (the computer predicted cleavage site is after Leu24), a 188 amino acid extracellular domain, a 21 amino acid transmembrane domain, and a 383 amino acid cytoplasmic tail. The extracellular region of RANK displayed significant amino acid homology (38.5% identity, 52.3% similarity) to CD40. A cloning vector (pBluescriptSK<sup>-</sup>) containing human RANK sequence, designated
- 20 pBluescript:huRANK (in *E. coli* DH10B), was deposited with the American Type Culture Collection, Rockville, MD (ATCC) on December 20, 1996, under terms of the Budapest Treaty, and given accession number 98285.

#### EXAMPLE 2

- 25 This example describes construction of a RANK DNA construct to express a RANK/Fc fusion protein. A soluble form of RANK fused to the Fc region of human IgG<sub>1</sub> was constructed in the mammalian expression vector pDC409 (USSN 08/571,579). This expression vector encodes the leader sequence of the Cytomegalovirus (CMV) open reading frame R27080 (SEQ ID NO:9), followed by amino acids 33-213 of RANK, followed by a
- 30 mutated form of the constant domain of human IgG<sub>1</sub> that exhibits reduced affinity for Fc receptors (SEQ ID NO:8; for the fusion protein, the Fc portion of the construct consisted of Arg3 through Lys232). An alternative expression vector encompassing amino acids 1-213 of RANK (using the native leader sequence) followed by the IgG<sub>1</sub> muin was also prepared. Both expression vectors were found to induce high levels of expression of the
- 35 RANK/Fc fusion protein in transfected cells.

To obtain RANK/Fc protein, a RANK/Fc expression plasmid is transfected into CV-1/EBNA cells, and supernatants are collected for about one week. The RANK/Fc fusion protein is purified by means well-known in the art for purification of Fc fusion

proteins, for example, by protein A sepharose column chromatography according to manufacturer's recommendations (i.e., Pharmacia, Uppsala, Sweden). SDS-polyacrylamide gel electrophoresis analysis indicated that the purified RANK/Fc protein migrated with a molecular weight of ~55kDa in the presence of a reducing agent, and at a molecular weight of ~110kDa in the absence of a reducing agent.

N-terminal amino acid sequencing of the purified protein made using the CMV R27080 leader showed 60% cleavage after Ala20, 20% cleavage after Pro22 and 20% cleavage after Arg28 (which is the Furin cleavage site; amino acid residues are relative to SEQ ID NO:9); N-terminal amino acid analysis of the fusion protein expressed with the native leader showed cleavage predominantly after Gln25 (80% after Gln25 and 20% after Arg23; amino acid residues are relative to SEQ ID NO:6, full-length RANK). Both fusion proteins were able to bind a ligand for RANK in a specific manner (i.e., they bound to the surface of various cell lines such as a murine thymoma cell line, EL4), indicating that the presence of additional amino acids at the N-terminus of RANK does not interfere with its ability to bind RANKL. Moreover, the construct comprising the CMV leader encoded RANK beginning at amino acid 33; thus, a RANK peptide having an N-terminus at an amino acid between Arg23 and Pro33, inclusive, is expected to be able to bind a ligand for RANK in a specific manner.

Other members of the TNF receptor superfamily have a region of amino acids between the transmembrane domain and the ligand binding domain that is referred to as a 'spacer' region, which is not necessary for ligand binding. In RANK, the amino acids between 196 and 213 are predicted to form such a spacer region. Accordingly, a soluble form of RANK that terminates with an amino acid in this region is expected to retain the ability to bind a ligand for RANK in a specific manner. Preferred C-terminal amino acids for soluble RANK peptides are selected from the group consisting of amino acids 213 and 196 of SEQ ID NO:6, although other amino acids in the spacer region may be utilized as a C-terminus.

#### EXAMPLE 3

This example illustrates the preparation of monoclonal antibodies against RANK. Preparations of purified recombinant RANK, for example, or transfected cells expressing high levels of RANK, are employed to generate monoclonal antibodies against RANK using conventional techniques, such as those disclosed in U.S. Patent 4,411,993. DNA encoding RANK can also be used as an immunogen, for example, as reviewed by Pardoll and Beckerleg in *Immunity* 3:165, 1995. Such antibodies are likely to be useful in interfering with RANK-induced signaling (antagonistic or blocking antibodies) or in inducing a signal by cross-linking RANK (agonistic antibodies), as components of

#### EXAMPLE 4

This example illustrates the induction of NF- $\kappa$ B activity by RANK in 293/EBNA cells (cell line was derived by transfection of the 293 cell line with a gene encoding Epstein-Barr virus nuclear antigen-1 (EBNA-1) that constitutively express EBNA-1 driven from human CMV immediate-early enhancer/promoter). Activation of NF- $\kappa$ B activity was measured in 293/EBNA cells essentially as described by Yao et al. (*Immunity* 3:811, 1995). Nuclear extracts were prepared and analyzed for NF- $\kappa$ B activity by a gel retardation assay using a 25 base pair oligonucleotide spanning the NF- $\kappa$ B binding sites. Two million cells were seeded into 10 cm dishes two days prior to DNA transfection and cultured in DMEM-F12 media containing 2.5% FBS (fetal bovine serum). DNA transfections were performed as described herein for the IL-8 promoter/reporter assays.

Nuclear extracts were prepared by solubilization of isolated nuclei with 400 mM NaCl (Yao et al., *supra*). Oligonucleotides containing an NF- $\kappa$ B binding site were annealed and endlabeled with  $^{32}$ P using T4 DNA polynucleotide kinase. Mobility shift reactions contained 10  $\mu$ g of nuclear extract, 4  $\mu$ g of poly(dI-dC) and 15,000 cpm labeled double-stranded oligonucleotide and incubated at room temperature for 20 minutes. Resulting protein-DNA complexes were resolved on a 6% native polyacrylamide gel in 0.25 X Tris-borate-EDTA buffer.

Overexpression of RANK resulted in induction of NF- $\kappa$ B activity as shown by an appropriate shift in the mobility of the radioactive probe on the gel. Similar results were observed when RANK was triggered by a ligand that binds RANK and transduces a signal to cells expressing the receptor (i.e., by co-transfecting cells with human RANK and murine RANKL DNA; see Example 7 below), and would be expected to occur when triggering is done with agonistic antibodies.

#### EXAMPLE 5

This example describes a gene promoter/reporter system based on the human Interleukin-8 (IL-8) promoter used to analyze the activation of gene transcription in vivo. The induction of human IL-8 gene transcription by the cytokines Interleukin-1 (IL-1) or tumor necrosis factor-alpha (TNF- $\alpha$ ) is known to be dependent upon intact NF- $\kappa$ B and NF-IL-6 transcription factor binding sites. Fusion of the cytokine-responsive IL-8 promoter with a cDNA encoding the murine IL-4 receptor (mIL-4R) allows measurement of promoter activation by detection of the heterologous reporter protein (mIL-4R) on the cell surface of transfected cells.

Human kidney epithelial cells (293/EBNA) are transfected (via the DEAE/Dextran method) with plasmids encoding: 1) the reporter/promoter construct (referred to as pIL-8rep), and 2) the cDNA(s) of interest. DNA concentrations are always kept constant by the addition of empty vector DNA. The 293/EBNA cells are plated at a



density of  $2.5 \times 10^4$  cells/ml (3 ml/well) in a 6 well plate and incubated for two days prior to transfection. Two days after transfection, the mIL-4 receptor is detected by a radioimmunoassay (RIA) described below.

In one such experiment, the 293/EBNA cells were co-transfected with DNA encoding RANK and with DNA encoding RANKL (see Example 7 below). Co-expression of this receptor and its counterstructure by cells results in activation of the signaling process of RANK. For such co-transfection studies, the DNA concentration/well for the DEAE transfection were as follows: 40 ng of pIL-8rep [pBluescriptSK<sup>-</sup> vector (Stratagene)]; 0.4 ng CD40 (DNA encoding CD40, a control receptor; pCDM8 vector); 0.4 ng RANK (DNA encoding RANK; pDC409 vector), and either 1-50 ng CD40L (DNA encoding the ligand for CD40, which acts as a positive control when co-transfected with CD40 and as a negative control when co-transfected with RANK; in pDC304) or RANKL (DNA encoding a ligand for RANK; in pDC406). Similar experiments can be done using soluble RANKL or agonistic antibodies to RANK to trigger cells transfected with RANK.

For the mIL-4R-specific RIA, a monoclonal antibody reactive with mIL-4R is labeled with  $^{125}$ I via a Chloramine T conjugation method; the resulting specific activity is typically  $1.5 \times 10^{16}$  cpm/nmol. After 48 hours, transfected cells are washed once with media (DMEM/F12 5% FBS). Non-specific binding sites are blocked by the addition of pre-warmed binding media containing 5% non-fat dry milk and incubation at  $37^\circ\text{C}/5\% \text{CO}_2$  in a tissue culture incubator for one hour. The blocking media is decanted and binding buffer containing  $^{125}$ I anti-mIL-4R (clone M1; rat IgG1) is added to the cells and incubated with rocking at room temperature for 1 hour. After incubation of the cells with the radio-labeled antibody, cells are washed extensively with binding buffer (2X) and twice with phosphate-buffered saline (PBS). Cells are lysed in 1 ml of 0.5M NaOH, and total radioactivity is measured with a gamma counter.

Using this assay, 293/EBNA co-transfected with DNAs encoding RANK demonstrated transcriptional activation, as shown by detection of mIL-4R on the cell surface. Overexpression of RANK resulted in transcription of mIL-4R, as did triggering of the RANK by RANKL. Similar results are observed when RANK is triggered by agonistic antibodies.

#### EXAMPLE 6

This example illustrates the association of RANK with TRAF proteins. Interaction of RANK with cytoplasmic TRAF proteins was demonstrated by co-immunoprecipitation assays essentially as described by Hsu et al. (*Cell* 84:299; 1996). Briefly, 293/EBNA cells were co-transfected with plasmids that direct the synthesis of RANK and epitope-tagged (FLAG $\alpha$ ; SEQ ID NO:7) TRAF2 or TRAF3. Two days after transfection, surface proteins

- were labeled with biotin-ester, and cells were lysed in a buffer containing 0.5% NP-40. RANK and proteins associated with this receptor were immunoprecipitated with anti-RANK, washed extensively, resolved by electrophoretic separation on a 6-10% SDS polyacrylamide gel and electrophoretically transferred to a nitrocellulose membrane for Western blotting. The association of TRAF2 and TRAF3 proteins with RANK was visualized by probing the membrane with an antibody that specifically recognizes the FLAG® epitope. TRAFs 2 and 3 did not immunoprecipitate with anti-RANK in the absence of RANK expression.

#### EXAMPLE 7

- This example describes isolation of a ligand for RANK, referred to as RANKL, by direct expression cloning. The ligand was cloned essentially as described in USSN 08/249,189, filed May 24, 1994 (the relevant disclosure of which is incorporated by reference herein), for CD40L. Briefly, a library was prepared from a clone of a mouse thymoma cell line EL-4 (ATCC TIB 39), called EL-40.5, derived by sorting five times with biotinylated CD40/Fc fusion protein in a FACS (fluorescence activated cell sorter). The cDNA library was made using standard methodology; the plasmid DNA was isolated and transfected into sub-confluent CV1-EBNA cells using a DEAE-dextran method. Transfectants were screened by slide autoradiography for expression of RANKL using a two-step binding method with RANK/Fc fusion protein as prepared in Example 2 followed by radiolabeled goat anti-human IgG antibody.

- A clone encoding a protein that specifically bound RANK was isolated and sequenced; the clone was referred to as 11H. An expression vector containing murine RANKL sequence, designated pDC406:muRANK-L (in *E. coli* DH10B), was deposited with the American Type Culture Collection, Rockville, MD (ATCC) on December 20, 1996, under terms of the Budapest Treaty, and given accession number 98284. The nucleotide sequence and predicted amino acid sequence of this clone are illustrated in SEQ ID NO:10. This clone did not contain an initiator methionine; additional, full-length clones were obtained from a 7B9 library (prepared substantially as described in US patent 5,599,905, issued February 4, 1997); the 5' region was found to be identical to that of human RANKL as shown in SEQ ID NO: 12, amino acids 1 through 22, except for substitution of a Gly for a Thr at residue 9.

- This ligand is useful for assessing the ability of RANK to bind RANKL by a number of different assays. For example, transfected cells expressing RANKL can be used in a FACS assay (or similar assay) to evaluate the ability of soluble RANK to bind RANKL. Moreover, soluble forms of RANKL can be prepared and used in assays that are known in the art (i.e., ELISA or BIAcore assays essentially as described in USSN 08/249,189, filed May 24, 1994). RANKL is also useful in affinity purification of RANK.

and as a reagent in methods to measure the levels of RANK in a sample. Soluble RANKL is also useful in inducing NF- $\kappa$ B activation and thus protecting cells that express RANK from apoptosis.

#### EXAMPLE 8

5 This example describes the isolation of a human RANK ligand (RANKL) using a PCR-based technique. Murine RANK ligand-specific oligonucleotide primers were used in PCR reactions using human cell line-derived first strand cDNAs as templates. Primers corresponded to nucleotides 478-497 and to the complement of nucleotides 858-878 of murine RANK ligand (SEQ ID NO:10). An amplified band approximately 400 bp in length from one reaction using the human epidermoid cell line KB (ATCC CCL-17) was gel purified, and its nucleotide sequence determined; the sequence was 85% identical to the corresponding region of murine RANK ligand, confirming that the fragment was from human RANKL.

To obtain full-length human RANKL cDNAs, two human RANKL-specific oligonucleotides derived from the KB PCR product nucleotide sequence were radiolabeled and used as hybridization probes to screen a human PBL cDNA library prepared in lambda gt10 (Stratagene, La Jolla, CA), substantially as described in US patent 5,599,905, issued February 4, 1997. Several positive hybridizing plaques were identified and purified, their inserts subcloned into pBluescript SK<sup>+</sup> (Stratagene, La Jolla, CA), and their nucleotide sequence determined. One isolate, PBL3, was found to encode most of the predicted human RANKL, but appeared to be missing approximately 200 bp of 5' coding region. A second isolate, PBL5 was found to encode much of the predicted human RANKL, including the entire 5' end and an additional 200 bp of 5' untranslated sequence.

The 5' end of PBL5 and the 3' end of PBL3 were ligated together to form a full length cDNA encoding human RANKL. The nucleotide and predicted amino acid sequence of the full-length human RANK ligand is shown in SEQ ID NO:12. Human RANK ligand shares 83% nucleotide and 84% amino acid identity with murine RANK ligand. A plasmid vector containing human RANKL sequence, designated pBluescript:huRANK-L (in *E. coli* DH10B), was deposited with the American Type Culture Collection, Rockville, MD (ATCC) on March 11, 1997 under terms of the Budapest Treaty, and given accession number 98354.

Murine and human RANKL are Type 2 transmembrane proteins. Murine RANKL contains a predicted 48 amino acid intracellular domain, 21 amino acid transmembrane domain and 247 amino acid extracellular domain. Human RANKL contains a predicted 47 amino acid intracellular domain, 21 amino acid transmembrane domain and 249 amino acid extracellular domain.

**EXAMPLE 9**

This example describes the chromosomal mapping of human RANK using PCR-based mapping strategies. Initial human chromosomal assignments were made using RANK and RANKL-specific PCR primers and a BIOS Somatic Cell Hybrid PCRable DNA kit from BIOS Laboratories (New Haven, CT), following the manufacturer's instructions. RANK mapped to human chromosome 18; RANK ligand mapped to human chromosome 13. More detailed mapping was performed using a radiation hybrid mapping panel Genebridge 4 Radiation Hybrid Panel (Research Genetics, Huntsville, AL; described in Walter, MA et al., *Nature Genetics* 7:22-28, 1994). Data from this analysis was then submitted electronically to the MIT Radiation Hybrid Mapper (URL: <http://www-genome.wi.mit.edu/cgi-bin/c-ontig/rhmapper.pl>) following the instructions contained therein. This analysis yielded specific genetic marker names which, when submitted electronically to the NCBI Entrez browser (URL: <http://www3.ncbi.nlm.nih.gov/htbin-post/Entrez/query?db=c&form=0>), yielded the specific map locations. RANK mapped to chromosome 18q22.1, and RANKL mapped to chromosome 13q14.

**EXAMPLE 10**

This example illustrates the preparation of monoclonal antibodies against RANKL. Preparations of purified recombinant RANKL, for example, or transfected cells expressing high levels of RANKL, are employed to generate monoclonal antibodies against RANKL using conventional techniques, such as those disclosed in US Patent 4,411,993. DNA encoding RANKL can also be used as an immunogen, for example, as reviewed by Pardoll and Beckerleg in *Immunology* 3:165, 1995. Such antibodies are likely to be useful in interfering with RANKL signaling (antagonistic or blocking antibodies), as components of diagnostic or research assays for RANKL or RANKL activity, or in affinity purification of RANKL.

To immunize rodents, RANKL immunogen is emulsified in an adjuvant (such as complete or incomplete Freund's adjuvant, alum, or another adjuvant, such as Ribi adjuvant R700 (Ribi, Hamilton, MT), and injected in amounts ranging from 10-100 µg subcutaneously into a selected rodent, for example, BALB/c mice or Lewis rats. DNA may be given intradermally (Raz et al., *Proc. Natl. Acad. Sci. USA* 91:9519, 1994) or intramuscularly (Wang et al., *Proc. Natl. Acad. Sci. USA* 90:4156, 1993); saline has been found to be a suitable diluent for DNA-based antigens. Ten days to three weeks days later, the immunized animals are boosted with additional immunogen and periodically boosted thereafter on a weekly, biweekly or every third week immunization schedule.

Serum samples are periodically taken by retro-orbital bleeding or tail-tip excision for testing by dot-blot assay (antibody sandwich), ELISA (enzyme-linked immunosorbent

assay), immunoprecipitation, or other suitable assays, including FACS analysis. Following detection of an appropriate antibody titer, positive animals are given an intravenous injection of antigen in saline. Three to four days later, the animals are sacrificed, splenocytes harvested, and fused to a murine myeloma cell line (e.g., NS1 or preferably Ag 8.653 [ATCC CRL 1580]). Hybridoma cell lines generated by this  
5 procedure are plated in multiple microtiter plates in a selective medium (for example, one containing hypoxanthine, aminopterin, and thymidine, or HAT) to inhibit proliferation of non-fused cells, myeloma-myeloma hybrids, and splenocyte-splenocyte hybrids.

- Hybridoma clones thus generated can be screened by ELISA for reactivity with  
10 RANKL, for example, by adaptations of the techniques disclosed by Engvall et al., *Immunochem.* 8:871 (1971) and in US Patent 4,703,004. A preferred screening technique is the antibody capture technique described by Beckman et al., *J. Immunol.* 144:4212 (1990). Positive clones are then injected into the peritoneal cavities of syngeneic rodents to produce ascites containing high concentrations (>1 mg/ml) of anti-RANK monoclonal  
15 antibody. The resulting monoclonal antibody can be purified by ammonium sulfate precipitation followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can also be used, as can affinity chromatography based upon binding to RANKL protein. Using the methods described herein to monitor the activity of the mAbs, both blocking (i.e.,  
20 antibodies that bind RANKL and inhibit binding to RANK) and non-blocking (i.e., antibodies that bind RANKL and do not inhibit binding) are isolated.

**EXAMPLE 11**

This example demonstrates that RANK expression can be up-regulated. Human peripheral blood T cells were purified by flow cytometry sorting or by negative selection using antibody coated beads, and activated with anti-CD3 (OKT3, Dako) coated plates or phytohemagglutinin in the presence or absence of various cytokines, including Interleukin-4 (IL-4), Transforming Growth Factor- $\beta$  (TGF- $\beta$ ) and other commercially available cytokines (IL-1- $\alpha$ , IL-2, IL-3, IL-6, IL-7, IL-8, IL-10, IL-12, IL-15, IFN- $\gamma$ , TNF- $\alpha$ ). Expression of RANK was evaluated by FACS in a time course experiment for day 2 to day 8, using a mouse monoclonal antibody mAb144 (prepared as described in Example 3), as shown in the table below. Results are expressed as '+' to '++++' referring to the relative increase in intensity of staining with anti-RANK. Double labeling experiments using both anti-RANK and anti-CD8 or anti-CD4 antibodies were also performed.

Table 1: Upregulation of RANK by Cytokines

Cytokine (concentration)	Results:
IL-4 (50 ng/ml)	+
TGF- $\beta$ (5 ng/ml)	+ to ++
IL-4 (50 ng/ml) + TGF- $\beta$ (5 ng/ml)	++++
IL-1- $\alpha$ (10ng/ml)	-
IL-2 (20ng/ml)	-
IL-3 (25ng/ml)	-
IL-7 (20ng/ml)	-
IL-8 (10ng/ml)	-
IL-10 (50ng/ml)	-
IL-12 (10ng/ml)	-
IL-15 (10ng/ml)	-
IFN- $\gamma$ (100U/ml)	-
TNF- $\alpha$ (10ng/ml)	-

Of the cytokines tested, IL-4 and TGF- $\beta$  increased the level of RANK expression on both CD8+ cytotoxic and CD4+ helper T cells from day 4 to day 8. The combination of IL-4 and TGF- $\beta$  acted synergistically to upregulate expression of this receptor on activated T cells. This particular combination of cytokines is secreted by suppressor T cells, and is believed to be important in the generation of tolerance (reviewed in Mitchison and Sieper, *Z. Rheumatol.* 54:141, 1995), implicating the interaction of RANK in regulation of an immune response towards either tolerance or induction of an active immune response.

### EXAMPLE 12

This example illustrates the influence of RANK.Fc and hRANKL on activated T cell growth. The addition of TGF $\beta$  to anti-CD3 activated human peripheral blood T lymphocytes induces proliferation arrest and ultimately death of most lymphocytes within the first few days of culture. We tested the effect of RANK:RANKL interactions on TGF $\beta$ -treated T cells by adding RANK.Fc or soluble human RANKL to T cell cultures.

Human peripheral blood T cells ( $7 \times 10^5$  PBT) were cultured for six days on anti-CD3 (OKT3, 5 $\mu$ g/ml) and anti-Flag (M1, 5 $\mu$ g/ml) coated 24 well plates in the presence of TGF $\beta$  (1ng/ml) and IL-4 (10ng/ml), with or without recombinant FLAG-tagged soluble hRANKL (1 $\mu$ g/ml) or RANK.Fc (10 $\mu$ g/ml). Viable T cell recovery was determined by triplicate trypan blue countings.

The addition of RANK.Fc significantly reduced the number of viable T cells recovered after six days, whereas soluble RANKL greatly increased the recovery of viable T cells (Figure 1). Thus, endogenous or exogenous RANKL enhances the number of viable T cells generated in the presence of TGF $\beta$ . TGF $\beta$ , along with IL-4, has been implicated in immune response regulation when secreted by the T $H$ 3/regulatory T cell subset. These T cells are believed to mediate bystander suppression of effector T cells. Accordingly, RANK and its ligand may act in an auto/paracrine fashion to influence T cell tolerance. Moreover, TGF $\beta$  is known to play a role in the evasion of the immune system effected by certain pathogenic or opportunistic organisms. In addition to playing a role in the development of tolerance, RANK may also play a role in immune system evasion by pathogens.

### EXAMPLE 13

This example illustrates the influence of the interaction of RANK on CD1a<sup>+</sup> dendritic cells (DC). Functionally mature dendritic cells (DC) were generated *in vitro* from CD34<sup>+</sup> bone marrow (BM) progenitors. Briefly, human BM cells from normal healthy volunteers were density fractionated using Ficoll medium and CD34<sup>+</sup> cells immunoaffinity isolated using an anti-CD34 matrix column (Ceptrate, CellPro). The CD34<sup>+</sup> BM cells were then cultured in human GM-CSF (20 ng/ml), human IL-4 (20 ng/ml), human TNF- $\alpha$  (20 ng/ml), human CHO-derived Flt3L (FL; 100 ng/ml) in Super McCoy's medium supplemented with 10% fetal calf serum in a fully humidified 37°C incubator (5% CO $_2$ ) for 14 days. CD1a<sup>+</sup>, HLA-DR<sup>+</sup> DC were then sorted using a FACStar Plus™, and used for biological evaluation of RANK.

On human CD1a<sup>+</sup> DC derived from CD34<sup>+</sup> bone marrow cells, only a subset (20-30%) of CD1a<sup>+</sup> DC expressed RANK at the cell surface as assessed by flow cytometric

analysis. However, addition of CD40L to the DC cultures resulted in RANK surface expression on the majority of CD1a<sup>+</sup> DC. CD40L has been shown to activate DC by enhancing *in vitro* cluster formation, inducing DC morphological changes and upregulating HLA-DR, CD54, CD58, CD80 and CD86 expression

- 5 Addition of RANKL to DC cultures significantly increased the degree of DC aggregation and cluster formation above control cultures, similar to the effects seen with CD40L (Figure 2). Sorted human CD1a<sup>+</sup> DC were cultured in a cytokine cocktail (GM-CSF, IL-4, TNF- $\alpha$  and FL) (upper left panel), in cocktail plus CD40L (1 $\mu$ g/ml) (upper right), in cocktail plus RANKL (1 $\mu$ g/ml) (lower left), or in cocktail plus heat inactivated (ΔH) RANKL (1 $\mu$ g/ml) (lower right) in 24-well flat bottomed culture plates in 1 ml culture media for 48-72 hours and then photographed using an inversion microscope. An increase in DC aggregation and cluster formation above control cultures was not evident when heat inactivated RANKL was used, indicating that this effect was dependent on biologically active protein. However, initial phenotypic analysis of adhesion molecule expression indicated that RANKL-induced clustering was not due to increased levels of CD2, CD11a, CD54 or CD58.

- The addition of RANKL to CD1a<sup>+</sup> DC enhanced their allo-stimulatory capacity in a mixed lymphocyte reaction (MLR) by at least 3- to 10-fold, comparable to CD40L-cultured DC (Figure 3). Allogeneic T cells (1x10<sup>5</sup>) were incubated with varying numbers of irradiated (2000 rad) DC cultured as indicated above for Figure 2 in 96-well round bottomed culture plates in 0.2 ml culture medium for four days. The cultures were pulsed with 0.5 mCi [<sup>3</sup>H]-thymidine for eight hours and the cells harvested onto glass fiber sheets for counting on a gas phase β counter. The background counts for either T cells or DC cultured alone were <100 cpm. Values represent the mean ± SD of triplicate cultures. Heat inactivated RANKL had no effect. DC allo-stimulatory activity was not further enhanced when RANKL and CD40L were used in combination, possibly due to DC functional capacity having reached a maximal level with either cytokine alone. Neither RANKL nor CD40L enhanced the *in vitro* growth of DC over the three day culture period. Unlike CD40L, RANKL did not significantly increase the levels of HLA-DR expression nor the expression of CD80 or CD86.

- RANKL can enhance DC cluster formation and functional capacity without modulating known molecules involved in cell adhesion (CD18, CD54), antigen presentation (HLA-DR) or costimulation (CD86), all of which are regulated by CD40/CD40L signaling. The lack of an effect on the expression of these molecules suggests that RANKL may regulate DC function via an alternate pathway(s) distinct from CD40/CD40L. Given that CD40L regulates RANK surface expression on *in vitro*-generated DC and that CD40L is upregulated on activated T cells during DC-T cell



interactions, RANK and its ligand may form an important part of the activation cascade that is induced during DC-mediated T cell expansion. Furthermore, culture of DC in RANKL results in decreased levels of CD11c expression, and increased levels of CD83. Both of these molecules are similarly modulated during DC maturation by CD40L (Caux et al. *J. Exp. Med.* 180:1263; 1994), indicating that RANKL induces DC maturation.

- 5 Dendritic cells are referred to as "professional" antigen presenting cells, and have a high capacity for sensitizing MHC-restricted T cells. There is growing interest in using dendritic cells *ex vivo* as tumor or infectious disease vaccine adjuvants (see, for example, Romani, et al., *J. Exp. Med.*, 180:83, 1994). Therefore, an agent such as RANKL that  
 10 induces DC maturation and enhances the ability of dendritic cells to stimulate an immune response is likely to be useful in immunotherapy of various diseases.

#### EXAMPLE 14

- This example describes the isolation of the murine homolog of RANK, referred to as muRANK. MuRANK was isolated by a combination of cross-species PCR and colony  
 15 hybridization. The conservation of Cys residues in the Cys-rich pseudorepeats of the extracellular domains of TNFR superfamily member proteins was exploited to design human RANK-based PCR primers to be used on murine first strand cDNAs from various sources. Both the sense upstream primer and the antisense downstream primer were  
 20 designed to have their 3' ends terminate within Cys residues.

- The upstream sense primer encoded nucleotides 272-295 of SEQ ID NO:5 (region encoding amino acids 79-86); the downstream antisense primer encoded the complement of nucleotides 409-427 (region encoding amino acids 124-130). Standard PCR reactions  
 25 were set up and run, using these primers and first strand cDNAs from various murine cell line or tissue sources. Thirty reaction cycles of 94°C for 30 seconds, 50°C for 30 seconds, and 72°C for 20 seconds were run. PCR products were analyzed by electrophoresis, and specific bands were seen in several samples. The band from one sample was gel purified and DNA sequencing revealed that the sequence between the primers was approximately  
 85% identical to the corresponding human RANK nucleotide sequence.

- A plasmid based cDNA library prepared from the murine fetal liver epithelium line FLE18 (one of the cell lines identified as positive in the PCR screen) was screened for full-length RANK cDNAs using murine RANK-specific oligonucleotide probes derived from the murine RANK sequence determined from sequencing the PCR product. Two cDNAs,  
 30 one encoding the 5' end and one encoding the 3' end of full-length murine RANK (based on sequence comparison with the full-length human RANK) were recombined to generate a full-length murine RANK cDNA. The nucleotide and amino acid sequence of muRANK are shown in SEQ ID Nos:14 and 15.

The cDNA encodes a predicted Type 1 transmembrane protein having 625 amino acid residues, with a predicted 30 amino acid signal sequence, a 184 amino acid extracellular domain, a 21 amino acid transmembrane domain, and a 390 amino acid cytoplasmic tail. The extracellular region of muRANK displayed significant amino acid homology (69.7% identity, 80.8% similarity) to huRANK. Those of skill in the art will recognize that the actual cleavage site can be different from that predicted by computer; accordingly, the N-terminal of RANK may be from amino acid 25 to amino acid 35.

Other members of the TNF receptor superfamily have a region of amino acids between the transmembrane domain and the ligand binding domain that is referred to as a 'spacer' region, which is not necessary for ligand binding. In muRANK, the amino acids between 197 and 214 are predicted to form such a spacer region. Accordingly, a soluble form of RANK that terminates with an amino acid in this region is expected to retain the ability to bind a ligand for RANK in a specific manner. Preferred C-terminal amino acids for soluble RANK peptides are selected from the group consisting of amino acids 214, and 197 of SEQ ID NO:14, although other amino acids in the spacer region may be utilized as a C-terminus.

#### EXAMPLE 15

This example illustrates the preparation of several different soluble forms of RANK and RANKL. Standard techniques of restriction enzyme cutting and ligation, in combination with PCR-based isolation of fragments for which no convenient restriction sites existed, were used. When PCR was utilized, PCR products were sequenced to ascertain whether any mutations had been introduced; no such mutations were found.

In addition to the huRANK/Fc described in Example 2, another RANK/Fc fusion protein was prepared by ligating DNA encoding amino acids 1-213 of SEQ ID NO:6, to DNA encoding amino acids 3-232 of the Fc muin described previously (SEQ ID NO:8). A similar construct was prepared for murine RANK, ligating DNA encoding amino acids 1-213 of full-length murine RANK (SEQ ID NO:15) to DNA encoding amino acids 3-232 of the Fc muin (SEQ ID NO:8).

A soluble, tagged, poly-His version of huRANKL was prepared by ligating DNA encoding the leader peptide from the immunoglobulin kappa chain (SEQ ID NO:16) to DNA encoding a short version of the FLAG™ tag (SEQ ID NO:17), followed by codons encoding Gly Ser, then a poly-His tag (SEQ ID NO:18), followed by codons encoding Gly Thr Ser, and DNA encoding amino acids 138-317 of SEQ ID NO:13. A soluble, poly-His tagged version of murine RANKL was prepared by ligating DNA encoding the CMV leader (SEQ ID NO:9) to codons encoding Arg Thr Ser, followed by DNA encoding poly-His (SEQ ID NO:18) followed by DNA encoding amino acids 119-294 of SEQ ID NO:11.

A soluble, oligomeric form of huRANKL was prepared by ligating DNA encoding the CMV leader (SEQ ID NO:9) to a codon encoding Asp followed by DNA ending a trimer-former "leucine" zipper (SEQ ID NO:19), then by codons encoding Thr Arg Ser followed by amino acids 138-317 of SEQ ID NO:13.

- 5 These and other constructs are prepared by routine experimentation. The various DNAs are then inserted into a suitable expression vector, and expressed. Particularly preferred expression vectors are those which can be used in mammalian cells. For example, pDC409 and pDC304, described herein, are useful for transient expression. For stable transfection, the use of CHO cells is preferred; several useful vectors are described in
- 10 USSN 08/785,150, now allowed, for example, one of the 2A5-3  $\lambda$ -derived expression vectors discussed therein.

#### EXAMPLE 16

- This example demonstrates that RANKL expression can be up-regulated on murine
- 15 T cells. Cells were obtained from mesenteric lymph nodes of C57BL/6 mice, and activated with anti-CD3 coated plates, Concanavalin A (ConA) or phorbol myristate acetate in combination with ionomycin (anti-CD3: 500A2; Immunex Corporation, Seattle WA; ConA, PMA, ionomycin, Sigma, St. Louis, MO) substantially as described herein, and cultured from about 2 to 5 days. Expression of RANKL was evaluated in a three color analysis by
- 20 FACS, using antibodies to the T cell markers CD4, CD8 and CD45RB, and RANK/Fc, prepared as described herein.

- RANKL was not expressed on unstimulated murine T cells. T cells stimulated with either anti-CD3, ConA, or PMA/ionomycin, showed differential expression of RANKL: CD4<sup>+</sup>/CD45RB<sup>Lo</sup> and CD4<sup>+</sup>/CD45RB<sup>Hi</sup> cells were positive for RANKL, but CD8<sup>+</sup> cells
- 25 were not. RANKL was not observed on B cells, similar to results observed with human cells.

#### EXAMPLE 17

- This example illustrates the effects of murine RANKL on cell proliferation and
- 30 activation. Various cells or cell lines representative of cells that play a role in an immune response (murine spleen, thymus and lymphnode) were evaluated by culturing them under conditions promoting their viability, in the presence or absence of RANKL. RANKL did not stimulate any of the tested cells to proliferate. One cell line, a macrophage cell line referred to as RAW 264.7 (ATCC accession number TIB 71) exhibited some signs of
- 35 activation.

RAW cells constitutively produce small amounts of TNF- $\alpha$ . Incubation with either human or murine RANKL enhanced production of TNF- $\alpha$  by these cells in a dose

- dependent manner. The results were not due to contamination of RANKL preparations with endotoxin, since boiling RANKL for 10 minutes abrogated TNF- $\alpha$  production, whereas a similar treatment of purified endotoxin (LPS) did not affect the ability of the LPS to stimulate TNF- $\alpha$  production. Despite the fact that RANKL activated the macrophage cell line RAW T64.7 for TNF- $\alpha$  production, neither human RANKL nor murine RANKL stimulated nitric oxide production by these cells.

#### EXAMPLE 18

- This example illustrates the effects of murine RANKL on growth and development of the thymus in fetal mice. Pregnant mice were injected with 1 mg of RANK/Fc or vehicle control protein (murine serum albumin; MSA) on days 13, 16 and 19 of gestation. After birth, the neonates continued to be injected with RANK/Fc intraperitoneally (IP) on a daily basis, beginning at a dose of 1  $\mu$ g, and doubling the dose about every four days, for a final dosage of 4  $\mu$ g. Neonates were taken at days 1, 8 and 15 post birth, their thymuses and spleens harvested and examined for size, cellularity and phenotypic composition.

- A slight reduction in thymic size at day 1 was observed in the neonates born to the female injected with RANK/Fc; a similar decrease in size was not observed in the control neonates. At day 8, thymic size and cellularity were reduced by about 50% in the RANK/Fc-treated animals as compared to MSA treated mice. Phenotypic analysis demonstrated that the relative proportions of different T cell populations in the thymus were the same in the RANK/Fc mice as the control mice, indicating that the decreased cellularity was due to a global depression in the number of thymic T cells as opposed to a decrease in a specific population(s). The RANK/Fc-treated neonates were not significantly different from the control neonates at day 15 with respect to either size, cellularity or phenotype of thymic cells. No significant differences were observed in spleen size, cellularity or composition at any of the time points evaluated. The difference in cellularity on day 8 and not on day 15 may suggest that RANK/Fc may assert its effect early in thymic development.

#### EXAMPLE 19

- This example demonstrates that the C-terminal region of the cytoplasmic domain of RANK is important for binding of several different TRAF proteins. RANK contains at least two recognizable PXQX(X)T motifs that are likely TRAF docking sites. Accordingly, the importance of various regions of the cytoplasmic domain of RANK for TRAF binding was evaluated. A RANK/GST fusion protein was prepared substantially as described in Smith and Johnson, *Gene* 67:31 (1988), and used in the preparation of various truncations as described below.

Comparison of the nucleotide sequence of murine and human RANK indicated that there were several conserved regions that could be important for TRAF binding. Accordingly, a PCR-based technique was developed to facilitate preparation of various C-terminal truncations that would retain the conserved regions. PCR primers were designed to introduce a stop codon and restriction enzyme site at selected points, yielding the truncations described in Table 1 below. Sequencing confirmed that no undesired mutations had been introduced in the constructs.

Radio-labeled (<sup>35</sup>S-Met, Cys) TRAF proteins were prepared by *in vitro* translation using a commercially available reticulocyte lysate kit according to manufacturer's instructions (Promega). Truncated GST fusion proteins were purified substantially as described in Smith and Johnson (supra). Briefly, *E. coli* were transfected with an expression vector encoding a fusion protein, and induced to express the protein. The bacteria were lysed, insoluble material removed, and the fusion protein isolated by precipitation with glutathione-coated beads (Sepahrose 4B, Pharmacia, Uppsala Sweden).

The beads were washed, and incubated with various radiolabeled TRAF proteins. After incubation and wash steps, the fusion protein/TRAF complexes were removed from the beads by boiling in 0.1% SDS + β-mercaptoethanol, and loaded onto 12% SDS gels (Novex). The gels were subjected to autoradiography, and the presence or absence of radiolabeled material recorded. The results are shown in Table 2 below.

Table 2: Binding of Various TRAF Proteins to the Cytoplasmic Domain of RANK

C terminal Truncations:	E206-S339	E206-Y421	E206-M476	E206-G544	Full length
TRAF1	-	-	-	-	++
TRAF2	-	-	-	-	++
TRAF3	-	-	-	-	++
TRAF4	-	-	-	-	-
TRAF5	-	-	-	-	+
TRAF6	-	+	+	+	++

These results indicate that TRAF1, TRAF2, TRAF3, TRAF 5 and TRAF6 bind to the most distal portion of the RANK cytoplasmic domain (between amino-acid G544 and A616). TRAF6 also has a binding site between S339 and Y421. In this experiment, TRAF5 also bound the cytoplasmic domain of RANK.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Immunex Corporation
- (ii) TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
- (iii) NUMBER OF SEQUENCES: 19
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Immunex Corporation, Law Department
  - (B) STREET: 51 University Street
  - (C) CITY: Seattle
  - (D) STATE: WA
  - (E) COUNTRY: USA
  - (F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: Apple Power Macintosh
  - (C) OPERATING SYSTEM: Apple Operating System 7.5.5
  - (D) SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE: 22 DECEMBER 1997
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US58 60/064,671
  - (B) FILING DATE: 14 OCTOBER 1997
  - (C) CLASSIFICATION:
- (viii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US58 08/813,509
  - (B) FILING DATE: 07 MARCH 1997
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US58 08/772,330 (60/064,671)
  - (B) FILING DATE: 23 DECEMBER 1996
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Perkins, Patricia Anne
  - (B) REGISTRATION NUMBER: 34,693
  - (C) REFERENCE/DOCKET NUMBER: 2852-WO
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (206)587-0430
  - (B) TELEFAX: (206)233-0644

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3115 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HOMO SAPIENS

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS

(B) CLONE: 9D-8A

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 93..1868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCTGCTGCTG	CTCTGCGGCG	TGCTGCGCCG	GCTGCAAGTTT	TATCCAGAAA	GAGCTGTGTG	60
GACTCTCTCG	CTGACCTCAG	TGTTCTTTTC	AG GTG	GCT TTG	CAG ATC	GCT CCT 113
				Val	Ala	Leu Gln Ile Ala Pro 1
CCA TCT	ACC AGT	GAG AAG	CAT TAT	GAG CAT	CTG GGA	COG TGC TGT AAC 161
Pro Cys	Thr Ser	Glu Lys	His Tyr	Glu His	Leu Gly	Arg Cys Cys Asn 10
						15 20
AAA TGT	GAA CCA	GGA AAG	TAC ATG	TCT TCT	AAA TGC	ACT ACT ACC TCT 209
Lys Cys	Glu Pro	Gly Lys	Tyr Met	Ser Ser	Lys Cys	Thr Thr Thr Ser 25
						30 35
GAC AGT	GTA TGT	CTG CCC	TGT GGC	CCG GAT	GAA TAC	TTG GAT AGC TGG 257
Asp Ser	Val Cys	Leu Pro	Cys Gly	Pro Asp	Glu Tyr	Leu Asp Ser Trp 40
						45 50 55
AAT GAA	GAA GAT	AAA TGC	TTG CTG	CAT AAA	GTT TGT	GAT ACA GGC AAG 305
Asn Glu	Glu Asp	Lys Cys	Leu Leu	His Lys	Val Cys	Asp Thr Gly Lys 60
						65 70
GCC CTG	GTG GCC	GTG GTC	GCC GGC	AAC AGC	ACG ACC	CCC COG CCG TGC 353
Ala Leu	Val Ala	Val Val	Ala Gly	Asn Ser	Thr Thr	Pro Arg Arg Cys 75
						80 85
GCG TGC	ACG GCT	GCG TAC	CAC TCG	AGC CAG	GAC TGC	GAG TGC TGC CCG 401
Ala Cys	Thr Ala	Gly Tyr	His Trp	Ser Gln	Asp Cys	Glu Cys Cys Arg 90
						95 100
GCG AAC	ACC GAG	TGC GCG	CCG GGC	CTG GGC	GGC CAG	CAC CCG TTG CAG 449
Arg Asn	Thr Glu	Cys Ala	Pro Gly	Leu Gly	Ala Gln	His Pro Leu Gln 105
						110 115
CTC AAC	AGG GAC	ACA GTG	TGC AAA	CGT TGC	CTT GCA	GGC TAC TTC TCT 497
Leu Asn	Lys Asp	Thr Val	Cys Lys	Pro Cys	Leu Ala	Gly Tyr Phe Ser 120
						125 130 135

GAT GCC TTT TCC TCC ACG GAC AAA TGC AGA CCC TGG ACC AAC TGT ACC Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr 140 145 150	545
TTC CTT GGA AAG AGA GTA GAA CAT CAT GGG ACA GAG AAA TCC GAT GCG Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala 155 160 165	593
GTT TGC AGT TCT TCT CTG CCA GGT AGA AAA CCA CCA AAT GAA CCC CAT Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His 170 175 180	641
GTT TAC TTG CCC GGT TTA ATA ATT CTG CTT CTC TTC GCG TCT GTG GCC Val Tyr Leu Pro Gly Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala 185 190 195	689
CTG GTG GCT GCC ATC ATC TTT GGC GTT TCC TAT AGG AAA GGG AAA Leu Val Ala Ala Ile Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys 200 205 210 215	737
GCA CTC ACA GCT AAT TTG TGG CAC TGG ATC AAT GAG GCT TGT GGC CCG Ala Leu Thr Ala Asn Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg 220 225 230	785
CTA AGT GGA GAT AAG GAG TCC TCA GGT GAC AGT TGT GTC AGT ACA CAC Leu Ser Gly Asp Lys Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His 235 240 245	833
ACG GCA AAC TTT GGT CAG CAG GGA GCA TGT GAA GGT GTC TTA CTG CTG Thr Ala Asn Phe Gly Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Leu 250 255 260	881
ACT CTG GAG GAG AAG ACA TTT CCA GAA GAT ATG TGC TAC CCA GAT CAA Thr Leu Glu Glu Lys Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln 265 270 275	929
GGT GGT GTC TGT CAG GGC ACG TGT GTA GGA GGT GGT CCC TAC GCA CAA Gly Gly Val Cys Gln Gly Thr Cys Val Gly Gly Pro Tyr Ala Gln 280 285 290 295	977
GGC GAA GAT GCC AGG ATG CTC TCA TTG CTC AGC AAG ACC GAG ATA GAG Gly Glu Asp Ala Arg Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu 300 305 310	1025
GAA GAC AGC TTC AGA CAG ATG CCC ACA GAA GAT GAA TAC ATG GAC AGC Glu Asp Ser Phe Arg Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg 315 320 325	1073
CCC TCC CAG CCC ACA GAC CAG TTA CTG TTC CTC ACT GAG CCT GGA AGC Pro Ser Gln Pro Thr Asp Gln Leu Leu Phe Leu Thr Thr Glu Pro Gly Ser 330 335 340	1121
AAA TCC ACA CCT CCT TTC TCT GAA CCC CTG GAG GTG GGG GAG AAT GAC Lys Ser Thr Pro Pro Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp 345 350 355	1169
AGT TTA AGC CAG TGC TTC ACG GGG ACA CAG AGC ACA GTG GGT TCA GAA Ser Leu Ser Gln Cys Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu 360 365 370 375	1217



AGC TGC AAC TGC ACT GAG CCC CTG TGC AGG ACT GAT TGG ACT CCC ATG Ser Cys Asn Cys Thr Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met 380 385 390	1265
TCC TCT GAA AAC TAC TTG CAA AAA GAG GTG GAC AGT GGC CAT TGC CCG Ser Ser Glu Asn Tyr Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro 395 400 405	1313
CAC TGG GCA GCC AGC CCC AGC CCC AAC TGG GCA GAT GTC TGC ACA GGC His Trp Ala Ala Ser Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly 410 415 420	1361
TGC CGG AAC CCT CCT GGG GAG GAC TGT GAA CCC CTC GTG GGT TCC CCA Cys Arg Asn Pro Pro Gly Glu Asp Cys Glu Pro Leu Val Gly Ser Pro 425 430 435	1409
AAA CCT GGA CCC TTG CCC CAG TGC GGC TAT GGC ATG GGC CTT CCC CCT Lys Arg Gly Pro Leu Pro Gln Cys Ala Tyr Gly Met Gly Leu Pro Pro 440 445 450	1457
GAA GAA GAA GCC AGC AGG ACG GAG GCC AGA GAC CAG CCC GAG GAT GGG Glu Glu Glu Ala Ser Arg Thr Glu Ala Arg Asp Gln Pro Glu Asp Gly 460 465 470	1505
GCT GAT GGG AGG CTC CCA AGC TCA CCG AGG GCA GGT GGC GGG TCT GGA Ala Asp Gly Arg Leu Pro Ser Ser Ala Arg Ala Gly Ala Gly Ser Gly 475 480 485	1553
AGC TCC CCT GGT GGC CAG TCC CCT GCA TCT GGA AAT GTG ACT GGA AAC Ser Ser Pro Gly Gly Gln Ser Pro Ala Ser Gly Asn Val Thr Gly Asn 490 495 500	1601
AGT AAC TCC AGC TTC ATC TCC AGC GGG CAG GTG ATG AAC TTC AAG GGC Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met Asn Phe Lys Gly 505 510 515	1649
GAC ATC ATC GTG GTC TAC GTC AGC CAG ACC TCG CAG GAG GGC GCG GCG Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln Glu Gly Ala Ala 520 525 530 535	1697
GCG GCT GCG GAG CCC ATG GGC CCG CCG GTG CAG GAG GAG ACC CTG GCG Ala Ala Ala Glu Pro Met Gly Arg Pro Val Gln Glu Glu Thr Leu Ala 540 545 550	1745
GCG CGA GAC TCC TTC GCG GGG AAC GGC CCG GCG TTC CCG GAC CCG TGC Arg Arg Asp Ser Phe Ala Gly Asn Gly Pro Arg Phe Pro Asp Pro Cys 555 560 565	1793
GCG GCG CCC GAG GGG CTG CCG GAG CCG GAG AAG GCG TCG AGG CCG GTG Gly Gly Pro Glu Gly Leu Arg Glu Pro Glu Lys Ala Ser Arg Pro Val 570 575 580	1841
CAG GAG CAA GGC GGG GGC AAG GCT TGA GCACCCCA TGGCTGGAG Gln Glu Gln Gly Gly Ala Lys Ala 585	1888
CCCGAAGCTC GGAGCCAGGG CTCGCGAGGG CAGCACCGCA GCTCTGCC CAGCCCGGC	1948
CACCCAGGGA TCGATCGGTA CAGTCGAGGA AGACCAACCC GCATCTCTCG CCCACTTTGC	2008
CTCCAGGAA ATGGGCTTT CAGGAAGTGA ATTGATGAGG ACTGTCCCA TGCCCAAGGA	2068

TGCTCAGCAG CCGCCGCAC TGGGGCAGAT GTCTCCCTG CCACCTCTCA AACTCGCAGC 2128  
 AGTAAATTGT GGCATATGA CAGTATTTT TATGACTATC CTGTTCTGTG GGGGGGGGGT 2188  
 CTATGTTTTC CCCCATATT TGTATTCCTT TTCATAACTT TTCTTGATAT CTTTCTCTCC 2248  
 TCTTTTAA TGTAAAGGTT TTCTCAAAA TTCTCTTAAA GGTGAGGGT TCTTTCTTTT 2308  
 CTCTTTTCTT TTTTCTTTC TTTTCTTGGC AACTTGCTC TGGCCCGAGC TAGAGTGCAG 2368  
 TGTGCGATT ATAGCCCGGT GCAGCTCTTA ACTCTGGGC TCAAGCAATC CAAGTGATCC 2428  
 TCCCACTCA ACCTTCGGAG TAGCTGGGAT CACAGCTGCA GGCACGCCC AGCTTCTTCC 2488  
 CCGGACTCC CCCCCCAG AGACACGCTC CCACCATGTT ACCCAGCCTG GTCTCAAACT 2548  
 CCCCAGCTAA AGCAGTCTC CAGCTCGGC CTCCCAAAGT ACTGGGATTA CAGGGGTGAG 2608  
 CCCCACGCT GGCCTGCTTT ACGTATTTTC TTTTGTCGCC CTGCTACAG TGTTTTAGAG 2668  
 ATGGCTTTC CAGTGTGTGT TCAATTGTAA CACTTTTGGG AAAGGGCTAA ACATGTGAGG 2728  
 CCTGGAGATA GTTCTAAGT TGCTAGGAAC ATGTGTGGG ACTTTCATAT TCTGAAAAAT 2788  
 GTTCTATATT CTCATTTTTC TAAAGGAAG AAAAAGGAA ACCCGATTTA TTCTCTCTGA 2848  
 ATCTTTTAA GTTGTGTCTG TTCTTAAGC AGAACTAAGC TCAGTATGTG ACCTTACCG 2908  
 CTAGGTGGTT AATTTATCCA TGCTGCGAGA GGCACCTCAGG TACTTGGTAA GCAAAATTCT 2968  
 AAAACTCCAA GTTCTGCGAG CTGCGCATTC TTCTTATTCT AGAGGTCTCT CTGAAAAAGA 3028  
 TGGAGAAAT GAACAGGACA TGGGCTCTCT GGAAGGAAG GGCCCGGAA GTTCAAGGAA 3088  
 GAATAAAGTT GAAATTTTAA AAAAAA 3115

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 591 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu Lys His Tyr Glu  
 1 5 10 15  
 His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly Lys Tyr Met Ser  
 20 25 30  
 Ser Lys Cys Thr Thr Thr Ser Asp Ser Val Cys Leu Pro Cys Gly Pro  
 35 40 45  
 Asp Glu Tyr Leu Asp Ser Thr Asn Glu Glu Asp Lys Cys Leu Leu His  
 50 55 60

Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val Val Ala Gly Asn  
 65 70 75 80  
 Ser Thr Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly Tyr His Trp Ser  
 85 90 95  
 Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys Ala Pro Gly Leu  
 100 105 110  
 Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr Val Cys Lys Pro  
 115 120 125  
 Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Ser Ser Thr Asp Lys Cys  
 130 135 140  
 Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg Val Glu His His  
 145 150 155 160  
 Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser Leu Pro Ala Arg  
 165 170 175  
 Lys Pro Pro Asn Glu Pro His Val Tyr Leu Pro Gly Leu Ile Ile Leu  
 180 185 190  
 Leu Leu Phe Ala Ser Val Ala Leu Val Ala Ala Ile Ile Phe Gly Val  
 195 200 205  
 Cys Tyr Arg Lys Lys Gly Lys Ala Leu Thr Ala Asn Leu Trp His Trp  
 210 215 220  
 Ile Asn Glu Ala Cys Gly Arg Leu Ser Gly Asp Lys Glu Ser Ser Gly  
 225 230 235 240  
 Asp Ser Cys Val Ser Thr His Thr Ala Asn Phe Gly Gln Gln Gly Ala  
 245 250 255  
 Cys Glu Gly Val Leu Leu Leu Thr Leu Glu Glu Lys Thr Phe Pro Glu  
 260 265 270  
 Asp Met Cys Tyr Pro Asp Gln Gly Gly Val Cys Gln Gly Thr Cys Val  
 275 280 285  
 Gly Gly Gly Pro Tyr Ala Gln Gly Glu Asp Ala Arg Met Leu Ser Leu  
 290 295 300  
 Val Ser Lys Thr Glu Ile Glu Glu Asp Ser Phe Arg Gln Met Pro Thr  
 305 310 315 320  
 Glu Asp Glu Tyr Met Asp Arg Pro Ser Gln Pro Thr Asp Gln Leu Leu  
 325 330 335  
 Phe Leu Thr Glu Pro Gly Ser Lys Ser Thr Pro Pro Phe Ser Glu Pro  
 340 345 350  
 Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln Cys Phe Thr Gly Thr  
 355 360 365  
 Gln Ser Thr Val Gly Ser Glu Ser Cys Asn Cys Thr Glu Pro Leu Cys  
 370 375 380

Arg Thr Asp Trp Thr Pro Met Ser Ser Glu Asn Tyr Leu Gln Lys Glu  
 385 390 395 400  
 Val Asp Ser Gly His Cys Pro His Trp Ala Ala Ser Pro Ser Pro Asn  
 405 410 415  
 Trp Ala Asp Val Cys Thr Gly Cys Arg Asn Pro Pro Gly Glu Asp Cys  
 420 425 430  
 Glu Pro Leu Val Gly Ser Pro Lys Arg Gly Pro Leu Pro Gln Cys Ala  
 435 440 445  
 Tyr Gly Met Gly Leu Pro Pro Glu Glu Glu Ala Ser Arg Thr Glu Ala  
 450 455 460  
 Arg Asp Gln Pro Glu Asp Gly Ala Asp Gly Arg Leu Pro Ser Ser Ala  
 465 470 475 480  
 Arg Ala Gly Ala Gly Ser Gly Ser Ser Pro Gly Gly Gln Ser Pro Ala  
 485 490 495  
 Ser Gly Asn Val Thr Gly Asn Ser Asn Ser Thr Phe Ile Ser Ser Gly  
 500 505 510  
 Gln Val Met Asn Phe Lys Gly Asp Ile Ile Val Tyr Val Ser Gln  
 515 520 525  
 Thr Ser Gln Glu Gly Ala Ala Ala Ala Glu Pro Met Gly Arg Pro  
 530 535 540  
 Val Gln Glu Glu Thr Leu Ala Arg Arg Asp Ser Phe Ala Gly Asn Gly  
 545 550 555 560  
 Pro Arg Phe Pro Asp Pro Cys Gly Gly Pro Glu Gly Leu Arg Glu Pro  
 565 570 575  
 Glu Lys Ala Ser Arg Pro Val Gln Glu Gln Gly Gly Ala Lys Ala  
 580 585 590

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1391 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: HOMO SAPIENS
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS
  - (B) CLONE: 9D-15C

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 39..1391

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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CCGCTGAGGC CGCGGCCGCC GCGAGCTGT CCGCGGCC ATG GCC CGC CGC GCC      53
                               Met Ala Pro Arg Ala
                               1      5
CGG CGC CGC CGC CGC CTG TTC GCG CTG CTG CTC TGC GCG CTG CTC      101
Arg Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu Cys Ala Leu Leu
10      15      20
GCC CGC CTG CAG GTG GCT TTG CAG ATC GCT CCT CCA TGT ACC AGT GAG      149
Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu
25      30      35
AAG CAT TAT GAG CAT CTG GGA CGG TGC TGT AAC AAA TGT GAA CCA GGA      197
Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly
40      45      50
AAG TAC ATG TCT TCT AAA TGC ACT ACT ACC TCT GAC AGT GTA TGT CTG      245
Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser Asp Ser Val Cys Leu
55      60      65
CCC TGT GGC CGC GAT GAA TAC TTG GAT AGC TGG AAT GAA GAA GAT AAA      293
Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp Asn Glu Glu Asp Lys
70      75      80      85
TGC TTG CTG CAT AAA GTT TGT GAT ACA GGC AAG GCC CTG GTG GCC GTG      341
Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val
90      95      100
CTC GCC GGC AAC AGC ACG ACC CCC CGG CCG TGC CGG TGC ACG GCT GGG      389
Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly
105      110      115
TAC CAC TGG AGC CAG GAC TGC GAG TGC TGC CGC CGC AAC ACC GAG TGC      437
Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys
120      125      130
GCG CGC GGC CTG GGC GCC CAG CAC CGG TTG CAG CTC AAC AAG GAC ACA      485
Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr
135      140      145
GTG TGC AAA CCT TGC CTT GCA GGC TAC TTC TCT GAT GCC TTT TCC TCC      533
Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Ser Ser
150      155      160      165
ACG GAC AAA TGC AGA CCC TGG ACC AAC TGT ACC TTC CTT GGA AAG AGA      581
Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg
170      175      180
GTA GAA CAT CAT GGG ACA GAG AAA TCC GAT CGC GTT TGC AGT TCT TCT      629
Val Glu His His Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser
185      190      195

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CTG CCA GCT AGA AAA CCA CCA AAT GAA CCC CAT GTT TAC TTG CCC GGT 677  
 Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His Val Tyr Leu Pro Gly  
 200 205 210

TTA ATA ATT CTG CTT CTC TTC GCG TCT GTG GCC CTG GTG GCT GCC ATC 725  
 Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala Leu Val Ala Ala Ile  
 215 220 225

ATC TTT GGC GTT TGC TAT AGG AAA AAA GGG AAA GCA CTC ACA GCT AAT 773  
 Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys Ala Leu Thr Ala Asn  
 230 235 240 245

TTG TGG CAC TGG ATC AAT GAG GCT TGT GGC GCG CTA AGT GGA GAT AAG 821  
 Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg Leu Ser Gly Asp Lys  
 250 255 260

GAG TCC TCA GGT GAC AGT TGT GTC AGT ACA CAC AGC GCA AAC TTT GGT 869  
 Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His Thr Ala Asn Phe Gly  
 265 270 275

CAG CAG GGA GCA TGT GAA GGT GTC TTA CTG CTG ACT CTG GAG GAG AAG 917  
 Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Leu Thr Leu Glu Glu Lys  
 280 285 290

ACA TTT CCA GAA GAT ATG TGC TAC CCA GAT CAA GGT GGT GTC TGT CAG 965  
 Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln Gly Gly Val Cys Gln  
 295 300 305

GGC ACG TGT GTA GGA GGT GGT CCC TAC GCA CAA GGC GAA GAT GCC AGG 013  
 Gly Thr Cys Val Gly Gly Gly Pro Tyr Ala Gln Gly Glu Asp Ala Arg  
 310 315 320 325

ATG CTC TCA TTG GTC AGC AAG ACC GAG ATA GAG GAA GAC AGC TTC AGA 061  
 Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu Glu Asp Ser Phe Arg  
 330 335 340

CAG ATG CCC ACA GAA GAT GAA TAC ATG GAC AGG CCC TCC CAG CCC ACA 109  
 Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg Pro Ser Gln Pro Thr  
 345 350 355

GAC CAG TTA CTG TTC CTC ACT GAG CTT GGA AGC AAA TCC ACA CCT CCT 157  
 Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser Lys Ser Thr Pro Pro  
 360 365 370

TTT TCT GAA CCC CTG GAG GTG GGG GAG AAT GAC AGT TTA AGC CAG TGC 205  
 Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln Cys  
 375 380 385

TTT ACG GGG ACA CAG AGC ACA GTG GGT TCA GAA AGC TGC AAC TGC ACT 253  
 Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu Ser Cys Asn Cys Thr  
 390 395 400 405

GAG CCC CTG TGC AGG ACT GAT TGG ACT CCC ATG TCC TCT GAA AAC TAC 301  
 Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met Ser Ser Glu Asn Tyr  
 410 415 420

TTG CAA AAA GAG GTG GAC AGT GGC CAT TGC CCG CAC TGG GCA GCC AGC 349  
 Leu Gln Lys Glu Val Asp Ser Lys His Cys Pro His Trp Ala Ala Ser  
 425 430 435

CCC ACC CCC AAC TGG GCA GAT GTC TGC ACA GGC TGC CGG AAC  
 Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly Cys Arg Asn  
 440 445 450

391

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 451 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Pro Arg Ala Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu  
 1 5 10 15  
 Leu Cys Ala Leu Leu Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro  
 20 25 30  
 Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn  
 35 40 45  
 Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser  
 50 55 60  
 Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp  
 65 70 75 80  
 Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys  
 85 90 95  
 Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys  
 100 105 110  
 Ala Cys Thr Ala Gly Tyr His Thr Ser Gln Asp Cys Glu Cys Cys Arg  
 115 120 125  
 Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln  
 130 135 140  
 Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser  
 145 150 155 160  
 Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr  
 165 170 175  
 Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala  
 180 185 190  
 Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His  
 195 200 205  
 Val Tyr Leu Pro Gly Leu Ile Leu Leu Leu Phe Ala Ser Val Ala  
 210 215 220  
 Leu Val Ala Ala Ile Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys  
 225 230 235 240

(2) INFORMATION FOR SEQ ID NO:5:

(A) LENGTH: 3136 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HOMO SAPIENS

(vii) IMMEDIATE SOURCE:



(A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS  
(B) CLONE: FULL LENGTH RANK

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 39..1886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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CCCGTGAGGC CCGGGCCCCC OCCAGCCTCT CCCGGGCC ATG GCC CCG CGC GCC      53
                                     Met Ala Pro Arg Ala
                                     1       5

CGG CGG CGC CGC CCG CTG TTC GCG CTG CTG CTG CTC TGC GCG CTG CTC      101
Arg Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu Cys Ala Leu Leu
                                     10       15       20

GCC CGG CTG CAG GTG GCT TTG CAG ATC GCT CCT CCA TGT ACC AGT GAG      149
Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu
                                     25       30       35

AAG CAT TAT GAG CAT CTG GGA GCG TGC TGT AAC AAA TGT GAA CCA GGA      197
Lys His Tyr Glu His Leu Gly Arg Cys Asn Lys Cys Glu Pro Gly
                                     40       45       50

AAG TAC ATG TCT TCT AAA TGC ACT ACT ACC TCT GAC AGT GTA TGT CTG      245
Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser Asp Ser Val Cys Leu
                                     55       60       65

CCC TGT GGC CGC GAT GAA TAC TTG GAT AGC TGG AAT GAA GAA GAT AAA      293
Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp Asn Glu Glu Asp Lys
                                     70       75       80       85

TGC TTG CTG CAT AAA GTT TGT GAT ACA GGC AAC GCC CTG GTG GCC GTG      341
Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val
                                     90       95       100

GTC GCC GGC AAC AGC ACG ACC CCC CGG CGC TGC GCG TGC ACG GCT GGG      389
Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly
                                     105       110       115

TAC CAC TGG AGC CAG GAC TGC GAG TGC TGC CCG CGC AAC ACC GAG TGC      437
Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys
                                     120       125       130

GCG CCG GGC CTG GGC GGC CAG CAC CCG TTG CAG CTC AAC AAG GAC ACA      485
Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr
                                     135       140       145

GTG TGC AAA CCT TGC CTT GCA GGC TAC TTC TCT GAT GCC TTT TCC TCC      533
Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser Ser Ala Phe Ser Ser
                                     150       155       160       165

ACG GAC AAA TGC AGA CCC TGG ACC AAC TGT ACC TTC CTT GGA AAG AGA      581
Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg
                                     170       175

GTA GAA CAT CAT GGG ACA GAG AAA TCC GAT GCG GTT TGC ACT TCT TCT      629
Val Glu His His Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser
                                     185       190       195

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CTG CCA GCT AGA AAA CCA CCA AAT GAA CCC CAT GTT TAC TTG CCC GGT Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His Val Tyr Leu Pro Gly 200 205 210	677
TTA ATA ATT CTG CTT CTC TTC GCG TCT GTG GCC CTG GTG GCT GCC ATC Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala Leu Val Ala Ala Ile 215 220 225	725
ATC TTT GGC GTT TGC TAT AGG AAA AAA GGG AAA GCA CTC ACA GCT AAT Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys Ala Leu Thr Ala Asn 230 235 240 245	773
TTG TGG CAC TGG ATC AAT GAG GCT TGT GGC CGC CTA AGT GGA GAT AAG Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg Leu Ser Gly Asp Lys 250 255 260	821
GAG TCC TCA GGT GAC AGT TOT GTC AGT ACA CAC ACG GCA AAC TTT GGT Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His Thr Ala Asn Phe Gly 265 270 275	869
CAG CAG GGA CCA TOT GAA GGT GTC TTA CTG CTG ACT CTG GAG GAC AAG Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Thr Leu Glu Glu Lys 280 285 290	917
ACA TTT CCA GAA GAT ATG TGC TAC CCA GAT CAA GGT GGT GTC TOT CAG Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln Gly Val Cys Gln 295 300 305	965
GGC ACG TOT GTA GGA GGT GGT CCC TAC CCA GAA GGC GAA GAT GGC AGG Gly Thr Cys Val Gly Gly Gly Pro Tyr Ala Gln Gly Glu Asp Ala Arg 310 315 320 325	1013
ATG CTC TCA TTG GTC AGC AAG ACC GAG ATA GAG GAA GAC AGC TTC AGA Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu Glu Asp Ser Phe Arg 330 335 340	1061
CAG ATG CCC ACA GAA GAT GAA TAC ATG GAC AGG CCC TCC CAG CCC ACA Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg Pro Ser Gln Pro Thr 345 350 355	1109
GAC CAG TTA CTG TTC CTC ACT GAG CCT GGA AGC AAA TCC ACA CCT CCT Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser Lys Ser Thr Pro Pro 360 365 370	1157
TTC TCT GAA CCC CTG GAG GTG GGG GAG AAT GAC AGT TTA AGC CAG TGC Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln Cys 375 380 385	1205
TTG ACG GGG ACA CAG AGC ACA GTG GGT TCA GAA AGC TGC AAC TGC ACT Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu Ser Cys Asn Cys Thr 390 395 400 405	1253
GAG CCC CTG TGC AGG ACT GAT TGG ACT CCC ATG TCC TCT GAA AAC TAC Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met Ser Ser Glu Asn Tyr 410 415 420	1301
TTG CAA AAA GAG GTG GAC AGT GGC CAT TGC CCG CAC TGG GCA GCC AGC Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro His Trp Ala Ala Ser 425 430 435	1349

CCC AGC CCC AAC TGG GCA GAT GTC TGC ACA GGC TCG CGG AAC CCT CCT 1397  
 Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly Cys Arg Asn Pro Pro  
 440 445 450

GGG GAG GAC TGT GAA CCC CTC GTG GGT TCC CCA AAA CGT GGA CCC TTG 1445  
 Gly Glu Asp Cys Glu Pro Leu Val Gly Ser Pro Lys Arg Gly Pro Leu  
 455 460 465

CCC CAG TGC GCC TAT GGC ATG GGC CTT CCC GAA GAA GAA GCC AGC 1493  
 Pro Gln Cys Ala Tyr Gly Met Gly Leu Pro Pro Glu Glu Glu Ala Ser  
 470 475 480 485

AGG ACG GAG GCC AGA GAC CAG CCC GAG GAT GGG GCT GAT GGG AGG CTC 1541  
 Arg Thr Glu Ala Arg Asp Gln Pro Glu Asp Gly Ala Asp Gly Arg Leu  
 490 495 500

CCA AGC TCA GCG AGG GCA GGT CCC GGG TCT GGA AGC TCC CCT GGT GGC 1589  
 Pro Ser Ser Ala Arg Ala Gly Ala Gly Ser Gly Ser Ser Pro Gly Gly  
 505 510 515

CAG TCC CCT GCA TCT GGA AAT GTG ACT GGA AAG AGT AAC TCC ACG TTC 1637  
 Gln Ser Pro Ala Ser Gly Asn Val Thr Gly Asn Ser Asn Ser Thr Phe  
 520 525 530

ATC TCC AGC GGG CAG GTG ATG AAC TTC AAG GGC GAC ATC ATC GTG GTC 1685  
 Ile Ser Ser Gly Gln Val Met Asn Phe Lys Gly Asp Ile Ile Val Val  
 535 540 545

TAC GTC AGC CAG ACC TCG CAG GAG GGC GCG GCG GCT GCG GAG CCC 1733  
 Tyr Val Ser Gln Thr Ser Gln Glu Gly Ala Ala Ala Ala Glu Pro  
 550 555 560 565

ATG GGC CCG CCG GTG CAG GAG GAG ACC CTG GCG CGC CGA GAC TCC TTC 1781  
 Met Gly Arg Pro Val Gln Glu Thr Leu Ala Arg Arg Asp Ser Phe  
 570 575 580

GCG GGG AAC GGC CCG CGC TTC CCG GAC CCG TGC GGC GGC CCC GAG GGG 1829  
 Ala Gly Asn Gly Pro Arg Phe Pro Asp Pro Cys Gly Gly Pro Glu Gly  
 585 590 595

CTG CCG GAG CCG GAG AAG GCC TCG AGG CCG GTG CAG GAG CAA GGC GGG 1877  
 Leu Arg Glu Pro Glu Lys Ala Ser Arg Pro Val Gln Glu Gln Gly Gly  
 600 605 610

GCC AAG GCT TGAGCGCCCC CCATGCTGG GAGCCCCAAG CTCGAGCCA 1926  
 Ala Lys Ala  
 615

GGCCTCGGA GGCAGCACC GCAGCCTCTG CCCCAGCCCC GACCACCAG GGATGATCG 1986

GTACAGTGA GGAAGACCAC CCGGCATCT CTGCCACTTT TGCTTCCAG GAAATGGCT 2046

TTTCAGGAAG TGAATGATG AGGACTGTCC CCATCCCCAC GGATGCTCAG CAGCCGCCG 2106

CACTGGGACA GATGTCTCCC CTGCCACTCC TCAACTCCG AGCAGTAATT TGTGGACTA 2166

TGACAGCTAT TTTTATGACT ATCTGTCTCT GTGGGGGGGG GGTCTATGTT TTCCCCCAT 2226

ATTGTATTC CTTTTCATAA CTTTCTCTGA TATCTTTCTT CCTCTTTTT TAAATGAAG 2286

GTTCTCTCAA AAATCTCTCT AAAGGTGAGG GTCTCTTCTT TTCTCTTTT CTTTTTTTT 2346

TTCTTTT TTTT GGCAACCTGG CTCTGGCCCA GGCTAGAGTG CAGTGGTGGC ATTATAGCCC 2406  
 GGTCAGCGCT CTAACCTCTG GGCTCAAGCA ATCCAAGTGA TCCTCCCACC TCAACCTTCC 2466  
 GAGTAGCTGG GATCACAGCT GCAGGCCACG CCCAGCTTCC TCCCCCGAC TCCCCCCCCC 2526  
 CAGGACACAG GTCCCAACAT GTTACCCAGC CTGGCTCTCA ACTCCCCAGC TAAAGCAGTC 2586  
 CTCCAGCCTC GGCTTCCCAA AGTACTGGGA TTACAGCGGT GAGCCCCACG GCTGGCCTGC 2646  
 TTTACGTATT TTCTTTTGTG CCCCCTGCTCA CAGTGTTTTA GAGATGGCTT TCCAGTGTG 2706  
 TGTTCAATTG AAACACTTTT GGGAAAGGGC TAAACATGTG AGGCCTGGAG ATAGTTGCTA 2766  
 AGTTGCTAGG AACATGTGTG GGGACTTTCA TATTCTGAAA AATGTTCTAT ATTCTCATTT 2826  
 TTCTAAAJA AAGAAAAAAG GAAACCCCAT TTATTCTCC TGAATCTTTT TAAGTTGTG 2886  
 TGCTTCTTA AGCAGAACTA AGCTCAGTAT GTGACCTTAC CCGCTAGGTG GTTAAATTAT 2946  
 CCATGCTGGC AGAGGCATC AGGTACTTGG TAAACAAATT TCTAAACTC CAACTTGTGC 3006  
 CAGCTTGCCA TTCTTCTTAT TCTAGAGGTC TCCTCTGAAA AGATOGAGAA AATGAACGG 3066  
 ACNTGGGGCT CTGGAAAGA AAGGGCCCCG GAAGTTCAAG GAAGAATAAA GTTGAATTTT 3126  
 TAAAAAANA 3136

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 616 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ala	Pro	Arg	Ala	Arg	Arg	Arg	Pro	Leu	Phe	Ala	Leu	Leu	Leu
1					5			10				15		
Leu	Cys	Ala	Leu	Leu	Ala	Arg	Leu	Gln	Val	Ala	Leu	Gln	Ile	Ala
		20					25					30		Pro
Pro	Cys	Thr	Ser	Glu	Lys	His	Tyr	Glu	His	Leu	Gly	Arg	Cys	Asn
		35					40					45		
Lys	Cys	Glu	Pro	Gly	Lys	Tyr	Met	Ser	Ser	Lys	Cys	Thr	Thr	Ser
		50				55					60			
Asp	Ser	Val	Cys	Leu	Pro	Cys	Gly	Pro	Asp	Glu	Tyr	Leu	Asp	Ser
	65				70				75				80	
Asn	Glu	Glu	Asp	Lys	Cys	Leu	Leu	His	Lys	Val	Cys	Asp	Thr	Gly
			85					90				95		Lys
Ala	Leu	Val	Ala	Val	Val	Ala	Gly	Asn	Ser	Thr	Thr	Pro	Arg	Arg
			100				105					110		Cys

Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg  
 115 120 125  
 Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln  
 130 135 140  
 Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser  
 145 150 155 160  
 Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr  
 165 170 175  
 Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala  
 180 185 190  
 Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His  
 195 200 205  
 Val Tyr Leu Pro Gly Leu Ile Ile Leu Leu Phe Ala Ser Val Ala  
 210 215 220  
 Leu Val Ala Ala Ile Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys  
 225 230 235 240  
 Ala Leu Thr Ala Asn Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg  
 245 250 255  
 Leu Ser Gly Asp Lys Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His  
 260 265 270  
 Thr Ala Asn Phe Gly Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Leu  
 275 280 285  
 Thr Leu Glu Glu Lys Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln  
 290 295 300  
 Gly Gly Val Cys Gln Gly Thr Cys Val Gly Gly Pro Tyr Ala Gln  
 305 310 315 320  
 Gly Glu Asp Ala Arg Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu  
 325 330 335  
 Glu Asp Ser Phe Arg Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg  
 340 345 350  
 Pro Ser Gln Pro Thr Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser  
 355 360 365  
 Lys Ser Thr Pro Pro Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp  
 370 375 380  
 Ser Leu Ser Gln Cys Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu  
 385 390 395 400  
 Ser Cys Asn Cys Thr Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met  
 405 410 415  
 Ser Ser Glu Asn Tyr Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro  
 420 425 430

His Trp Ala Ala Ser Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly  
 435 440 445  
 Cys Arg Asn Pro Pro Gly Glu Cys Glu Pro Leu Val Gly Ser Pro  
 450 455 460  
 Lys Arg Gly Pro Leu Pro Gln Cys Ala Tyr Gly Met Gly Leu Pro Pro  
 465 470 475 480  
 Glu Glu Glu Ala Ser Arg Thr Glu Ala Arg Asp Gln Pro Glu Asp Gly  
 485 490 495  
 Ala Asp Gly Arg Leu Pro Ser Ser Ala Arg Ala Gly Ala Gly Ser Gly  
 500 505 510  
 Ser Ser Pro Gly Gly Gln Ser Pro Ala Ser Gly Asn Val Thr Gly Asn  
 515 520 525  
 Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met Asn Phe Lys Gly  
 530 535 540  
 Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln Glu Gly Ala Ala  
 545 550 555 560  
 Ala Ala Ala Glu Pro Met Gly Arg Pro Val Gln Glu Thr Leu Ala  
 565 570 575  
 Arg Arg Asp Ser Phe Ala Gly Asn Gly Pro Arg Phe Pro Asp Pro Cys  
 580 585 590  
 Gly Gly Pro Glu Gly Leu Arg Glu Pro Glu Lys Ala Ser Arg Pro Val  
 595 600 605  
 Gln Glu Gln Gly Gly Ala Lys Ala  
 610 615

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDNESS: not relevant
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: FLAG® peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp Tyr Lys Asp Asp Asp Asp Lys  
 1 5

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 232 amino acids
  - (B) TYPE: amino acid

(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Human

(vii) IMMEDIATE SOURCE:  
(B) CLONE: IgG1 Fc mutein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

Glu Pro Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1           5           10           15
Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20           25           30
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35           40           45
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50           55           60
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65           70           75           80
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85           90           95
Asp Trp Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala
 100          105          110
Leu Pro Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115          120          125
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130          135          140
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg
 145          150          155          160
His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165          170          175
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180          185          190
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195          200          205
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210          215          220
Ser Leu Ser Leu Ser Pro Gly Lys
 225          230

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## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: CMV (R2780 Leader)
- (ix) FEATURE:
  - (D) OTHER INFORMATION: Met1-Arg28 is the actual leader peptide; Arg29 strengthens the furin cleavage site; nucleotides encoding Thr30 and Ser31 add a SpeI site.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:  

Met	Ala	Arg	Arg	Leu	Trp	Ile	Leu	Ser	Leu	Ala	Val	Thr	Leu	Thr
1					5				10				15	
Val	Ala	Leu	Ala	Ala	Pro	Ser	Gln	Lys	Ser	Lys	Arg	Arg	Thr	Ser
				20				25					30	

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1630 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Mus musculus
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY:
  - (B) CLONE: RANKL
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 3..884
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:



CC GGC GTC CCA CAC GAG GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro	47
1 5 10 15	
GCT CCG GCG CCG CCA CCC GCC GCC TCC GCG TCC ATG TTC CTG GCC CTC Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu	95
20 25 30	
CTG GGG CTG GGA CTG GGC CAG GTG GTC TCC AGC ATC GCT CTG TTC CTG Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu	143
35 40 45	
TAC TTT CGA GCG CAG ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr	191
50 55 60	
CAC TGC TTT TAT AGA ATC CTG AGA CTC CAT GAA AAC GCA GAT TTG CAG His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Asp Leu Gln	239
65 70 75	
GAC TCG ACT CTG CAG AGT GAA GAC ACA CTA CCT GAC TCC TCG AGG AGG Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg	287
80 85 90 95	
ATG AAA CAA GCC TTT CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile	335
100 105 110	
GTG GGG CCA CAG CCG TTC TCA GGA CCT CCA GCT ATG ATG GAA GGC TCA Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser	383
115 120 125	
TGG TTG GAT GTG GCC CAG CGA GGC AAG CCT GAG GCC CAG CCA TTT GCA Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala	431
130 135 140	
CAC CTC ACC ATC AAT GCT GCC AGC ATC CCA TCG GGT TCC CAT AAA GTC His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val	479
145 150 155	
ACT CTG TCC TCT TGG TAC CAC GAT CGA GGC TGG GCC AAG ATC TCT AAC Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn	527
160 165 170 175	
ATG ACG TTA AGC AAC CGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr	575
180 185 190	
TAC CTG TAC GCC AAC ATT TGC TTT CCG CAT CAT GAA ACA TCG GGA AGC Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser	623
195 200 205	
GTA CCT ACA GAC TAT CTT CAG CTG ATG GTG TAT GTC GTT AAA ACC AGC Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser	671
210 215 220	
ATC AAA ATC ACA AGT TCT CAT AAC CTG ATG AAA GGA GCG AGC ACG AAA Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys	719
225 230 235	

AAC TGG TCG GGC AAT TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG 767  
 Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly  
 240 245 250 255  
 GGA TTT TTC AAG CTC CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC 815  
 Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser  
 260 265 270  
 AAC CCT TCC CTG CTG GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT 863  
 Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala  
 275 280 285  
 TTC AAA GTT CAG GAC ATA GAC TGAGACTCAT TTGCTGGAAC ATTAGCATGG 914  
 Phe Lys Val Gln Asp Ile Asp  
 290  
 ATGTCTTAGA TGTTCGAAA CTTCCTAAAA AATGATGAT GTCTATACAT GTGTAAAGACT 974  
 ACTAAGAGAC ATGKCCACG GTGTATGAAA CTCACAGCCC TCTCTCTGCA GCTGTACAG 1034  
 GPTGTGTATA TGTAAAGTCC ATAGGTGATG TTAGATTCAT GGTGATTACA CAACGGTTTT 1094  
 ACAATTTTAT AATGATTTCG TAGAATTGAA CCAGATTGGG AGAGGTATTC CGATGCTTAT 1154  
 GAAAACTTA CAGGTGAGCT ATGGAAGGGG GTCACAGTCT CTGGGTCTAA CCCTGAGACA 1214  
 TGTGCCACTG AGAACCTTGA AATTAGAGG ATGCCATGTC ATTGCAAAGA AATGATAGTG 1274  
 TGAAGGGTTA AGTTCTTTTG AATTGTTACA TTGCCCTGGG ACCTGCAAAAT AAGTCTTTTT 1334  
 TTTCTAATGA GAGAGAAAA ATATATGTAT TTTTATATAA TGCTTAAAGT TATATTTCAG 1394  
 GTGTAATGTT TTCTGTGCAA AGTTTGTGTA ATTATATTG TGCTATAGTA TTGATTCAA 1454  
 AATATTAAAA AATGCTCAC TGTGACATA TTTAATGTTT TAAATGTACA GATGATTTTA 1514  
 ACTGCTGAC TTTGTAATTC CCTGAAGGT ACTGTAGCT AAGGGGGGAC AATACTGTTT 1574  
 CTGCTGACCA CATGTAGTTT ATTTCCTTAT TCTTTTAAAC TTAATAGAGT CTTCAG 1630

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 294 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala  
 1 5 10 15  
 Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu  
 20 25 30  
 Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr  
 35 40 45

Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His  
 50 55 60  
 Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Asp Leu Gln Asp  
 65 70 75 80  
 Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met  
 85 90 95  
 Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val  
 100 105 110  
 Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp  
 115 120 125  
 Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His  
 130 135 140  
 Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr  
 145 150 155 160  
 Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met  
 165 170 175  
 Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr  
 180 185 190  
 Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val  
 195 200 205  
 Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile  
 210 215 220  
 Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn  
 225 230 235 240  
 Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly  
 245 250 255  
 Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn  
 260 265 270  
 Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe  
 275 280 285  
 Lys Val Gln Asp Ile Asp  
 290

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 954 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE: huRANKL (full length)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG	CCC	GCC	GCC	AGC	AGA	GAC	TAC	ACC	AAG	TAC	CTG	CCT	GCC	TCG	GAG	48
Met	Arg	Arg	Ala	Ser	Arg	Asp	Tyr	Thr	Lys	Tyr	Leu	Arg	Gly	Ser	Glu	
1				5					10					15		
GAG	ATG	GCC	GCC	GCC	CCC	GGA	GCC	CCG	CAC	GAG	GCC	CCC	CTG	CAC	GCC	96
Glu	Met	Gly	Gly	Gly	Pro	Gly	Ala	Pro	His	Gly	Gly	Pro	Leu	His	Ala	
				20				25					30			
CCG	CCG	CCG	CCT	GCG	CCG	CAC	CAG	CCC	CCC	GCC	GCC	TCC	CCG	TCC	ATG	144
Pro	Pro	Pro	Pro	Ala	Pro	His	Gln	Pro	Pro	Ala	Ala	Ser	Arg	Ser	Met	
			35				40					45				
TTC	GTG	GCC	CTC	CTG	GGG	CTG	GGG	CTG	GCC	GAT	GTC	TGC	AGC	GTC		192
Phe	Val	Ala	Leu	Leu	Gly	Leu	Gly	Leu	Gly	Gln	Val	Val	Cys	Ser	Val	
			50			55					60					
GCC	CTG	TTC	TTC	TAT	TTC	AGA	GCG	CAG	ATG	GAT	CCT	AAT	AGA	ATA	TCA	240
Ala	Leu	Phe	Phe	Tyr	Phe	Arg	Ala	Gln	Met	Asp	Pro	Asn	Arg	Ile	Ser	
			65			70				75				80		
GAA	GAT	GGC	ACT	CAC	TGC	ATT	TAT	AGA	ATT	TTG	AGA	CTC	CAT	GAA	AAT	288
Glu	Asp	Gly	Thr	His	Cys	Ile	Tyr	Arg	Ile	Leu	Arg	Leu	His	Glu	Asn	
				85				90					95			
GCA	GAT	TTT	CAA	GAC	ACA	ACT	CTG	GAG	AGT	CAA	GAT	ACA	AAA	TTA	ATA	336
Ala	Asp	Phe	Gln	Asp	Thr	Thr	Leu	Glu	Ser	Gln	Asp	Thr	Lys	Leu	Ile	
			100					105					110			
CCT	GAT	TCA	TGT	AGG	AGA	ATT	AAA	CAG	GCC	TTT	CAA	GGA	GCT	GTG	CAA	384
Pro	Asp	Ser	Cys	Arg	Arg	Ile	Lys	Gln	Ala	Phe	Gln	Gly	Ala	Val	Gln	
			115			120						125				
AAG	GAA	TTA	CAA	CAT	ATC	GTT	GGA	TCA	CAG	CAC	ATC	AGA	GCA	GAG	AAA	432
Lys	Glu	Leu	Gln	His	Ile	Val	Gly	Ser	Gln	His	Ile	Arg	Ala	Glu	Lys	
			130			135					140					
GCG	ATG	GTG	GAT	GCG	TCA	TGG	TTA	GAT	CTG	GCC	AAG	AGG	AGC	AAG	CTT	480
Ala	Met	Val	Asp	Gly	Ser	Trp	Leu	Asp	Leu	Ala	Lys	Arg	Ser	Lys	Leu	
			145			150					155			160		
GAA	GCT	CAG	CCT	TTT	GCT	CAT	CTC	ACT	ATT	AAT	GCC	ACC	GAC	ATC	CCA	528
Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Thr	Asp	Ile	Pro	
				165				170						175		

TCT GGT TCC CAT AAA GTG AGT CTG TCC TCT TGG TAC CAT GAT CGG GGT Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly 180 185 190	576
TGG GCC AAG ATC TCC AAC ATG ACT TTT AGC AAT GGA AAA CTA ATA GTT Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val 195 200 205	624
AAT CAG GAT GGC TTT TAT TAC CTG TAT GCC AAC ATT TGC TTT CGA CAT Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His 210 215 220	672
CAT GAA ACT TCA GGA GAC CTA GCT ACA GAG TAT CTT CAA CTA ATG GTG His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val 225 230 235	720
TAC GTC ACT AAA ACC AGC ATC AAA ATC CCA AGT TCT CAT ACC CTG ATG Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met 240 245 250 255	768
AAA GGA GGA ACC ACC AAG TAT TGG TCA GGG AAT TCT GAA TTC CAT TTT Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe 260 265 270	816
TAT TCC ATA AAC GTT GGT GGA TTT TTT AAG TTA CGG TCT CGA GAG GAA Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu 275 280 285	864
ATC AGC ATC GAG GTC TCC AAC CCC TCC TTA CTG GAT CCG GAT CAG GAT Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp 290 295 300	912
GCA ACA TAC TTT GGG GCT TTT AAA GTT CGA GAT ATA GAT TGA Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp 305 310 315	954

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 317 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu  
1 5 10 15  
 Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala  
20 25 30  
 Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met  
35 40 45  
 Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val  
50 55 60

Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser  
 65 70 75 80  
 Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn  
 85 90 95  
 Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile  
 100 105 110  
 Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln  
 115 120 125  
 Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys  
 130 135 140  
 Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu  
 145 150 155 160  
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro  
 165 170 175  
 Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly  
 180 185 190  
 Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val  
 195 200 205  
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His  
 210 215 220  
 His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val  
 225 230 235 240  
 Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met  
 245 250 255  
 Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe  
 260 265 270  
 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu  
 275 280 285  
 Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp  
 290 295 300  
 Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp  
 305 310 315

## (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1878 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Murine

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Murine Petal Liver Epithelium

(B) CLONE: muRANK

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

ATG GCC CCG CCG GCC CGG CGG CGC CGC CAG CTG CCC GCG CCG CTG CTG 48
Met Ala Pro Arg Ala Arg Arg Arg Arg Gln Leu Pro Ala Pro Leu Leu
1 5 10 15
CGC CTC TGC CTC CTG CTC GTT CCA CTG CAG GTG ACT CTC CAG GTC ACT 96
Ala Leu Cys Val Leu Leu Val Pro Leu Gln Val Thr Leu Gln Val Thr
20 25 30
CCT CCA TGC ACC CAG GAG AGG CAT TAT GAG CAT CTC GGA CGG TGT TGC 144
Pro Pro Cys Thr Gln Glu Arg His Tyr Glu His Leu Gly Arg Cys Cys
35 40 45
AGC AGA TGC GAA CCA CCA AAG TAC CTG TCC TCT AAG TGC ACT CCT ACC 192
Ser Arg Cys Glu Pro Gly Lys Tyr Leu Ser Ser Lys Cys Thr Pro Thr
50 55 60
TCC GAC AGT GTG TGT CTG CCC TGT GGC CCC GAT GAG TAC TTG GAC ACC 240
Ser Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Thr
65 70 75 80
TGG AAT GAA GAA GAT AAA TGC TTG CTG CAT AAA GCT TGT GAT GCA GGC 288
Trp Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Ala Gly
85 90 95
AAG GCC CTG GTG CCG GTG GAT CCT GGC AAC CAC ACG GCC CCG COT CCG 336
Lys Ala Leu Val Ala Val Asp Pro Gly Asn His Thr Ala Pro Arg Arg
100 105 110
TOT GCT TGC ACG GCT GGC TAC CAC TGG AAC TCA GAC TGC GAG TGC TGC 384
Cys Ala Cys Thr Ala Gly Tyr His Trp Asn Ser Ser Asp Cys Glu Cys Cys
115 120 125
CGC AGG AAC ACG GAG TGT GCA CCT GGC TTC GGA GCT CAG CAT CCC TTG 432
Arg Arg Asn Thr Glu Cys Ala Pro Gly Phe Gly Ala Gln His Pro Leu
130 135 140
CAG CTC AAC AAG GAT ACG GTG TGC ACA CCC TGC CTC CTG GGC TTC TTC 480
Gln Leu Asn Lys Asp Thr Val Cys Thr Pro Cys Leu Leu Gly Phe Phe
145 150 155 160
TCA GAT GTC TTT TGC TCC ACA GAC AAA TGC AAA CCT TGG ACC AAC TGC 528
Ser Asp Val Phe Ser Ser Thr Asp Lys Cys Lys Pro Trp Thr Asn Cys
165 170 175

```

ACC CTC CTT GGA AAG CTA GAA GCA CAC CAG GGG ACA ACG GAA TCA GAT 576  
 Thr Leu Leu Gly Lys Leu Glu Ala His Gln Gly Thr Thr Glu Ser Asp  
 180 185 190

GTG GTC TGC AGC TCT TCC ATG ACA CTG AGG AGA CCA CCC AAG GAG GCC 624  
 Val Val Cys Ser Ser Ser Met Thr Leu Arg Arg Pro Pro Lys Glu Ala  
 195 200 205

CAG GCT TAC CTG CCC AGT CTC ATC GTT CTG CTC CTC TTC ATC TCT GTG 672  
 Gln Ala Tyr Leu Pro Ser Leu Ile Val Leu Leu Leu Phe Ile Ser Val  
 210 215 220

GTA GTA GTG GCT GCC ATC ATC TTC GGC GTT TAC TAC AGG AAG GGA GGC 720  
 Val Val Val Ala Ala Ile Ile Phe Gly Val Tyr Tyr Arg Lys Gly Gly  
 225 230 235 240

AAA GCG CTG ACA GCT AAT TTG TGG AAT TGG CTC AAT GAT GCT TGC AGT 768  
 Lys Ala Leu Thr Ala Asn Leu Trp Asn Trp Val Asn Asp Ala Cys Ser  
 245 250 255

AGT CTA AGT GGA AAT AAG GAG TCC TCA GGG GAC CGT TGT OCT GGT TCC 816  
 Ser Leu Ser Gly Asn Lys Glu Ser Ser Gly Asp Arg Cys Ala Gly Ser  
 260 265 270

CAC TCG GCA ACC TCC AGT CAG CAA GAA GTG TOT GAA GGT ATC TTA CTA 864  
 His Ser Ala Thr Ser Ser Gln Gln Glu Val Cys Glu Gly Ile Leu Leu  
 275 280 285

ATG ACT CGG GAG GAG AAG ATG GTT CCA GAA GAC GGT OCT GGA GTC TGT 912  
 Met Thr Arg Glu Glu Lys Met Val Pro Glu Asp Gly Ala Gly Val Cys  
 290 295 300

GGG CCT GFG TOT GCG GCA GGT GGG CCC TGG GCA GAA GTC AGA GAT TCT 960  
 Gly Pro Val Cys Ala Ala Gly Gly Pro Trp Ala Glu Val Arg Asp Ser  
 305 310 315 320

AGG ACG TTC ACA CTG GTC AGC GAG GTT GAG ACG CAA GGA GAC CTC TCG 1008  
 Arg Thr Phe Thr Leu Val Ser Glu Val Glu Thr Gln Gly Asp Leu Ser  
 325 330 335

AGG AAG ATT CCC ACA GAG GAT GAG TAC ACG GAC GCG CCC TCG CAG CCT 1056  
 Arg Lys Ile Pro Thr Glu Asp Glu Tyr Thr Asp Arg Pro Ser Gln Pro  
 340 345 350

TCG ACT GGT TCA CTG CTC CTA ATC CAG CAG GGA AGC AAA TCT ATA CCC 1104  
 Ser Thr Gly Ser Leu Leu Leu Ile Gln Gln Gly Ser Lys Ser Ile Pro  
 355 360 365

CCA TTC CAG GAG CCC CTG GAA GTG GGG GAG AAC GAC AGT TTA AGC CAG 1152  
 Pro Phe Gln Glu Pro Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln  
 370 375 380

TOT TTC ACC GGG AGT GAA AGC ACG GTG GAT TCT GAG GGC TOT GAC TTC 1200  
 Cys Phe Thr Gly Thr Glu Ser Thr Val Asp Ser Glu Gly Cys Asp Phe  
 385 390 395 400

ACT GAG CCT CCG AGC AGA ACT GAC TCT ATG CCC GTG TCC CCT GAA AAG 1248  
 Thr Glu Pro Pro Ser Arg Thr Asp Ser Met Pro Val Ser Pro Glu Lys  
 405 410 415



CAC CTG ACA AAA GAA ATA GAA GGT GAC AGT TGC CTC CCC TGG GTG GTC 1296  
His Leu Thr Lys Glu Ile Glu Gly Asp Ser Cys Leu Pro Trp Val Val  
420 425 430  
AGC TCC AAC TCA ACA GAT GGC TAC ACA GGC AGT GGG AAC ACT CCT GGG 1344  
Ser Ser Asn Ser Thr Asp Gly Tyr Thr Gly Ser Gly Asn Thr Pro Gly  
435 440 445  
GAG GAC CAT GAA CCC TTT CCA GGG TCC CTG AAA TOT GGA CCA TTG CCC 1392  
Glu Asp His Glu Pro Phe Pro Gly Ser Leu Lys Cys Gly Pro Leu Pro  
450 455 460  
CAG TGT GCC TAC AGC ATG GGC TTT CCC AGT GAA GCA GCA GCC AGC ATG 1440  
Gln Cys Ala Tyr Ser Met Gly Phe Pro Ser Glu Ala Ala Ala Ser Met  
465 470 475 480  
GCA GAG CGC GGA GTA CGG CCC CAG GAC AGG GCT GAT GAG AGG GGA GCC 1488  
Ala Glu Ala Gly Val Arg Pro Gln Asp Arg Ala Asp Glu Arg Gly Ala  
485 490 495  
TCA GGG TCC GGG AGC TCC CCC AGT GAC CAG CCA CCT GCC TCT GGG AAC 1536  
Ser Gly Ser Gly Ser Ser Pro Ser Asp Gln Pro Pro Ala Ser Gly Asn  
500 505 510  
GTG ACT GGA AAC AGT AAC TCC ACG TTC ATC TCT AGC GGG CAG GTG ATG 1584  
Val Thr Gly Asn Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met  
515 520 525  
AAC TTC AAG GGT GAC ATC ATC GTG GTG TAT GTC AGC CAG ACC TCG CAG 1632  
Asn Phe Lys Gly Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln  
530 535 540  
GAG GGC CCG GGT TCC GCA GAG CCC GAG TCG GAG CCC GTG GGC CCG CCT 1680  
Glu Gly Pro Gly Ser Ala Glu Pro Glu Ser Glu Pro Val Gly Arg Pro  
545 550 555 560  
GTG CAG GAG GAG ACG CTG GCA CAC AGA GAC TCC TTT GCG GGC ACC GCG 1728  
Val Gln Glu Glu Thr Leu Ala His Arg Asp Ser Phe Ala Gly Thr Ala  
565 570 575  
CCG CCG TTC CCC GAG GTC TOT GCC ACC GGG GCT GCG GTG CAG GAG CAG 1776  
Pro Arg Phe Pro Asp Val Cys Ala Thr Gly Ala Gly Leu Gln Glu Gln  
580 585 590  
GGG GCA CCC CGG CAG AAG GAC GGG ACA TCG CGG CCG GTG CAG GAG CAG 1824  
Gly Ala Pro Arg Gln Lys Asp Gly Thr Ser Arg Pro Val Gln Glu Gln  
595 600 605  
GGT GGG GCG CAG ACT TCA CTC CAT ACC CAG GGG TCC GGA CAA TOT GCA 1872  
Gly Gly Ala Gln Thr Ser Leu His Thr Gln Gly Ser Gly Gln Cys Ala  
610 615 620  
GAA TGA 1878  
625

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 625 amino acids

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

Met Ala Pro Arg Ala Arg Arg Arg Gln Leu Pro Ala Pro Leu Leu
 1           5           10           15
Ala Leu Cys Val Leu Leu Val Pro Leu Gln Val Thr Leu Gln Val Thr
 20           25           30
Pro Pro Cys Thr Gln Glu Arg His Tyr Glu His Leu Gly Arg Cys Cys
 35           40           45
Ser Arg Cys Glu Pro Gly Lys Tyr Leu Ser Ser Lys Cys Thr Pro Thr
 50           55           60
Ser Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Thr
 65           70           75           80
Trp Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Ala Gly
 85           90           95
Lys Ala Leu Val Ala Val Asp Pro Gly Asn His Thr Ala Pro Arg Arg
100           105           110
Cys Ala Cys Thr Ala Gly Tyr His Trp Asn Ser Asp Cys Glu Cys Cys
115           120           125
Arg Arg Asn Thr Glu Cys Ala Pro Gly Phe Gly Ala Gln His Pro Leu
130           135           140
Gln Leu Asn Lys Asp Thr Val Cys Thr Pro Cys Leu Leu Gly Phe Phe
145           150           155           160
Ser Asp Val Phe Ser Ser Thr Asp Lys Cys Lys Pro Trp Thr Asn Cys
165           170           175
Thr Leu Leu Gly Lys Leu Glu Ala His Gln Gly Thr Thr Glu Ser Asp
180           185           190
Val Val Cys Ser Ser Ser Met Thr Leu Arg Arg Pro Pro Lys Glu Ala
195           200           205
Gln Ala Tyr Leu Pro Ser Ser Leu Ile Val Leu Leu Phe Ile Ser Val
210           215           220
Val Val Val Ala Ala Ile Ile Phe Gly Val Tyr Tyr Arg Lys Gly Gly
225           230           235           240
Lys Ala Leu Thr Ala Asn Leu Trp Asn Trp Val Asn Asp Ala Cys Ser
245           250           255
Ser Leu Ser Gly Asn Lys Glu Ser Ser Gly Asp Arg Cys Ala Gly Ser
260           265           270
His Ser Ala Thr Ser Ser Gln Gln Glu Val Cys Glu Gly Ile Leu Leu
275           280           285

```

Met Thr Arg Glu Glu Lys Met Val Pro Glu Asp Gly Ala Gly Val Cys  
 290 295 300

Gly Pro Val Cys Ala Ala Gly Gly Pro Trp Ala Glu Val Arg Asp Ser  
 305 310 315 320

Arg Thr Phe Thr Leu Val Ser Glu Val Glu Thr Gln Gly Asp Leu Ser  
 325 330 335

Arg Lys Ile Pro Thr Glu Asp Glu Tyr Thr Asp Arg Pro Ser Gln Pro  
 340 345 350

Ser Thr Gly Ser Leu Leu Leu Ile Gln Gln Gly Ser Lys Ser Ile Pro  
 355 360 365

Pro Phe Gln Glu Pro Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln  
 370 375 380

Cys Phe Thr Gly Thr Glu Ser Thr Val Asp Ser Glu Gly Cys Asp Phe  
 385 390 395 400

Thr Glu Pro Pro Ser Arg Thr Asp Ser Met Pro Val Ser Pro Glu Lys  
 405 410 415

His Leu Thr Lys Glu Ile Glu Gly Asp Ser Cys Leu Pro Trp Val Val  
 420 425 430

Ser Ser Asn Ser Thr Asp Gly Tyr Thr Gly Ser Gly Asn Thr Pro Gly  
 435 440 445

Glu Asp His Glu Pro Phe Pro Gly Ser Leu Lys Cys Gly Pro Leu Pro  
 450 455 460

Gln Cys Ala Tyr Ser Met Gly Phe Pro Ser Glu Ala Ala Ser Met  
 465 470 475 480

Ala Glu Ala Gly Val Arg Pro Gln Asp Arg Ala Asp Glu Arg Gly Ala  
 485 490 495

Ser Gly Ser Gly Ser Ser Pro Ser Asp Gln Pro Pro Ala Ser Gly Asn  
 500 505 510

Val Thr Gly Asn Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met  
 515 520 525

Asn Phe Lys Gly Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln  
 530 535 540

Glu Gly Pro Gly Ser Ala Glu Pro Glu Ser Glu Pro Val Gly Arg Pro  
 545 550 555 560

Val Gln Glu Glu Thr Leu Ala His Arg Asp Ser Phe Ala Gly Thr Ala  
 565 570 575

Pro Arg Phe Pro Asp Val Cys Ala Thr Gly Ala Gly Leu Gln Glu Gln  
 580 585 590

Gly Ala Pro Arg Gln Lys Asp Gly Thr Ser Arg Pro Val Gln Glu Gln  
 595 600 605

Gly Gly Ala Gln Thr Ser Leu His Thr Gln Gly Ser Gly Gln Cys Ala  
610 615 620  
Glu  
625

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Trp Val Pro  
1 5 10 15  
Gly Ser Thr Gly  
20

## (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Asp Tyr Lys Asp Glu  
5

## (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

His His His His His His  
5

## (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 amino acids  
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SDQ ID NO:19:

Arg	Met	Lys	Gln	Ile	Glu	Asp	Lys	Ile	Glu	Glu	Ile	Leu	Ser	Lys	Ile
1					5				10				15		
Tyr	His	Ile	Glu	Asn	Glu	Ile	Ala	Arg	Ile	Lys	Lys	Leu	Ile	Gly	Glu
			20					25					30		

Arg

25

30

1

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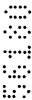
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(b) a DNA encoding a protein having an amino acid sequence as set forth in SEQ ID NO: 12, wherein the protein has an amino terminus selected from the group consisting of an amino acid 69 and amino acid 162, inclusive, and a carboxy terminus selected from the group consisting of an amino acid 313 and amino acid 317, inclusive;

(c) DNA molecules capable of hybridization to the DNA of (a) or (b) under stringent conditions, and which encode biologically active RANKL; and

(d) DNA molecules encoding fragments of proteins encoded by the DNA of (a), (b) or (c).

10



5. The isolated DNA of claim 4, which further comprises a DNA encoding a polypeptide selected from the group consisting of an immunoglobulin Fc domain, an immunoglobulin Fc mutein, a FLAG<sup>TM</sup> tag, a peptide comprising at least about 6 His residues, a leucine zipper, and combinations thereof.

15

6. A recombinant expression vector comprising a DNA sequence according to any one of claims 1 to 6.



20

7. A host cell transformed or transfected with an expression vector according to claim 6.



25

8. A process for preparing a RANKL protein, comprising culturing a host cell according to claim 7 under conditions promoting expression and recovering the RANKL.

9. An isolated DNA selected from the group consisting of oligonucleotides of at least about 17 nucleotides in length, oligonucleotides of at least about 25 nucleotides in length, and oligonucleotides of at least about 30 nucleotides in length, which is a fragment of the DNA of SEQ ID NO: 10 or SEQ ID NO: 12.

30

10. An isolated RANKL polypeptide selected from the group consisting of:



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16. A method of inducing maturation of dendritic cells (DC), comprising contacting CD1a + DC with an amount of a RANKL polypeptide sufficient to result in decreased levels of CD1b/c expression on the DC, under conditions promoting viability of the DC, and allowing the DC to mature.
- 5
17. A method of enhancing allo-stimulatory capacity in dendritic cells (DC), comprising contacting CD1a + DC with an amount of a RANKL polypeptide sufficient to increase the allo-stimulatory capacity of the DC in a mixed lymphocyte reaction (MLR), under conditions promoting viability of the DC, and allowing the DC to present antigens to T cells.
- 10
18. A method of promoting viability of T cells in the presence of TGF $\beta$ , comprising contacting T cells that have been exposed to TGF $\beta$  with an amount of a RANKL polypeptide sufficient to increase the number of T cells that remain viable in the presence of TGF $\beta$ , under conditions that would promote viability of T cells in the absence of TGF $\beta$ , and allowing the T cells to influence T cell tolerance.
- 15
19. An isolated DNA according to claim 1, substantially as hereinbefore described.
- 20
20. A recombinant expression vector according to claim 6, substantially as hereinbefore described.
- 25
21. A host cell according to claim 7, substantially as hereinbefore described.
22. A polypeptide according to claim 10, substantially as hereinbefore described.
- 30
23. An antibody according to claim 14, substantially as hereinbefore described.
24. A method according to claim 16, substantially as hereinbefore described.



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26. A method according to claim 18, substantially as hereinbefore described.

5

PHILLIPS ORMONDE &amp; FITZPATRICK

IMMUNEX CORPORATION



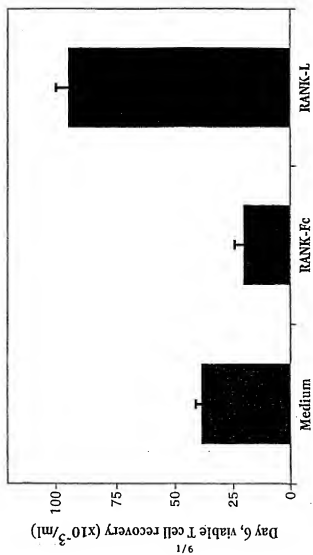
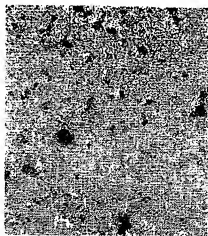
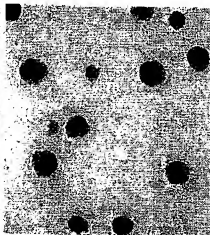
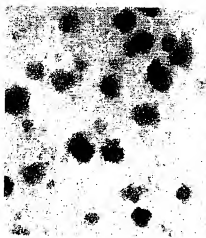
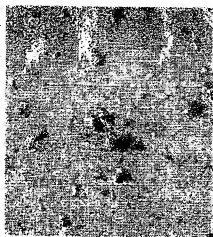


Figure 1

*Fig. 2A**Fig. 2B**Fig. 2C**Fig. 2D*

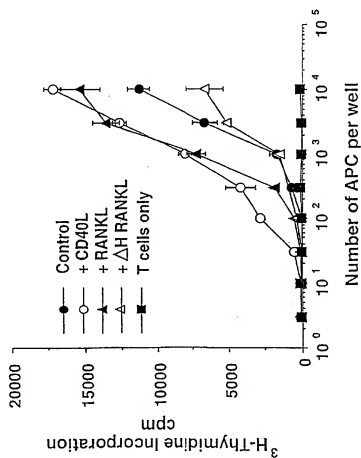


Figure 3





**Figure 5 (cont.)**



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